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OM nucleic - nucleic search, using sw model

Run on: May 10, 2005, 16:50:43 ; Search time 279.152 Seconds
(without alignments)
9724.375 Million cell updates/sec

Title: US-10-044-205A-3
Perfect score: 1659
Sequence: 1 atgttgacatggggccct.....ctggcgtgtttgtattg 1659

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1655.8	99.8	2249	US-09-802-117-5	Sequence 5, Appli
2	1655.8	99.8	2249	US-10-217-745-5	Sequence 5, Appli
3	1655.4	99.8	1662	US-09-802-117-1	Sequence 1, Appli
4	1655.4	99.8	1662	US-10-217-745-1	Sequence 1, Appli
5	1654.2	99.7	1662	US-09-738-894A-1	Sequence 1, Appli
6	1654.2	99.7	1662	US-09-964-469-1	Sequence 1, Appli
7	1046.8	63.1	1062	US-09-802-117-3	Sequence 3, Appli
8	1046.8	63.1	1062	US-10-217-745-3	Sequence 3, Appli
9	617.4	37.2	3651	US-09-738-894A-3	Sequence 3, Appli
10	617.4	37.2	3651	US-09-964-469-3	Sequence 3, Appli
11	419.8	25.3	2848	US-08-464-954A-2	Sequence 2, Appli
12	418.2	25.2	2204	US-08-221-817-12	Sequence 12, Appli
13	418.2	25.2	2204	US-08-454-439-12	Sequence 12, Appli
14	418.2	25.2	2204	PCT-US94-10487-12	Sequence 12, Appli
15	395.8	23.9	1983	US-08-221-817-21	Sequence 21, Appli
16	395.8	23.9	1983	US-08-454-439-21	Sequence 21, Appli
17	395.8	23.9	1983	PCT-US94-10487-21	Sequence 21, Appli
18	389.4	23.5	2206	US-08-221-817-10	Sequence 10, Appli
19	389.4	23.5	2206	US-08-454-439-10	Sequence 10, Appli
20	389.4	23.5	2206	PCT-US94-10487-10	Sequence 10, Appli
21	373	22.5	2511	US-09-417-197-60	Sequence 60, Appli
22	373	22.5	2529	US-09-417-197-42	Sequence 42, Appli
23	373	22.5	2557	US-09-016-434-1298	Sequence 1298, Ap
24	366.6	22.1	2557	US-08-464-954A-1	Sequence 1, Appli
25	320.6	19.3	2017	US-09-614-748A-8	Sequence 8, Appli
26	320.6	19.3	2113	US-09-614-748A-7	Sequence 7, Appli
27	311.6	18.8	1879	US-09-614-748A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-09-802-117-5
; Sequence 5, Application US/09802117
; Patent No. 644456

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wilganowski, Nathaniel L.

; TITLE OF INVENTION: Turner, C. Alexander Jr.

; FILE REFERENCE: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu

; CURRENT APPLICATION NUMBER: US/09/802.117

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 60/188,449

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 2249

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-802-117-5

Query Match	99.8%;	Score 1655.8;	DB 3;	Length 2249;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1657;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	ATGCTGGACATGGGGGCCCTGGACAACTGATCGCAACACCGCTACTCGAGGCCCGG	60	
Db	354	ATGCTGGACATGGGGGCCCTGGACAACTGATCGCAACACCGCTACTCGAGGCCCGG	413	
Qy	61	AAGCCCTCGGACTCGGACAGCAAGAGCTGCGAGGGGGGGGGGGGGGGGGGGGGGGGG	120	
Db	414	AAGCCCTCGGACTCGGACAGCAAGAGCTGCGAGGGGGGGGGGGGGGGGGGGGGGGGG	473	
Qy	121	GGGCTGAGGGCTGG	180	
Db	474	GGGCTGAGGGCTGG	533	
Qy	181	GAGCAGCAGCCCATCGGTCGGCGGCTCTTCGGTGACTTCCTAGCCACAGTGCACAGTTC	240	
Db	534	GAGCAGCAGCCCATCGGTCGGCGGCTCTTCGGTGACTTCCTAGCCACAGTGCACAGTTC	593	
Qy	241	CGCAAGCGCGCAACTTCCTTAGAGAGCAGTGGAGAGTGGCGAGTGGCGAGGAGGCC	300	
Db	594	CGCAAGCGCGCAACTTCCTTAGAGAGCAGTGGAGAGTGGCGAGTGGCGAGGAGGCC	653	
Qy	301	ACCAAGACAGCGCGCTGCGAGGGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCGGG	360	
Db	654	ACCAAGACAGCGCGCTGCGAGGGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCGGG	713	

QY	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTTATGACAAA	1500
Db	1794	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTTATGACAAA	1853
QY	1501	GATAAGCAGTCTCTCAAAAACCTTTGCGACAGGTGCTGTTCTATAGCATGCGCAGGAAGA	1560
Db	1854	GATAAGCAGTCTCTCAAAAACCTTTGCGACAGGTGCTGTTCTATAGCATGCGCAGGAAGA	1913
QY	1561	ATTATAGAACCGGACTGTTGAGGAACCTGATGATGACCCCAACAGACCTACCGGTTGTGAG	1620
Db	1914	ATTATAGAACCGGACTGTTGAGGAACCTGATGATGACCCCAACAGACCTACCGGTTGTGAG	1973
QY	1621	GAGGGTAATTCATCAAGTCTGCGGTGTTGTTTATTG	1659
Db	1974	GAGGGTAATTCATCAAGTCTGCGGTGTTGTTTATTG	2012
RESULT 2			
US-10-217-745-5			
; Sequence 5, Application US/10217745			
; Patent No. 6838275			
; GENERAL INFORMATION:			
; APPLICANT: Walke, D. Wade			
; APPLICANT: Wilganowski, Nathaniel L.			
; APPLICANT: Turner, C. Alexander Jr.			
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and			
; TITLE OF INVENTION: Polynucleotides			
; TITLE OF INVENTION: Encoding the Same			
; FILE REFERENCE: LEX-0147-USA			
; CURRENT APPLICATION NUMBER: US/10/217,745			
; CURRENT FILING DATE: 2002-08-12			
; PRIOR APPLICATION NUMBER: US/09/802,117			
; PRIOR FILING DATE: 2001-03-08			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 5			
; LENGTH: 2249			
; TYPE: DNA			
; ORGANISM: homo sapiens			
US-10-217-745-5			
Query Match 99.8%; Score 1655.8; DB 4; Length 2249;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	ATGFTGACATGCGGGCCCTGGACAACTGATGCGCAACACCGCTACCTGACGCGCGG	60
Db	354	ATGFTGACATGCGGGCCCTGGACAACTGATGCGCAACACCGCTACCTGACGCGCGG	413
QY	61	AAGCCCTCGGACTGCGACGACAAAGAGCTGCGCGGGCGGCGGTAGCTGGCCCTGCC	120
Db	414	AAGCCCTCGGACTGCGACGACAAAGAGCTGCGCGGGCGGCGGTAGCTGGCCCTGCC	473
QY	121	GCGCTGACAGGCTGCGCGGAGCTCGCGAGAGCTCGCGAGAGCTGCGGAGCTGCTGAACTTCCACAGCTGT	180
Db	474	GCGCTGACAGGCTGCGCGGAGCTCGCGAGAGCTCGCGAGAGCTGCGGAGCTGCTGAACTTCCACAGCTGT	533
QY	181	GAGCAGAGCCCATCGCTGCGCGCTCTTCCTGAGCTTCTTAGCCACAGTGCCTGCGGCGG	240
Db	534	GAGCAGAGCCCATCGCTGCGCGCTCTTCCTGAGCTTCTTAGCCACAGTGCCTGCGGCGG	593
QY	241	CGCAAGCGGGCAACCTTCTTAGAGGACGTGCGAGAACTGGAGCTGGCGAGGAGGACCC	300
Db	594	CGCAAGCGGGCAACCTTCTTAGAGGACGTGCGAGAACTGGAGCTGGCGAGGAGGACCC	653
QY	301	ACCAAGACAGCGCTGCGCGGCTGGCGCTTGTGCGAGTGCCTGCGCGCGG	360
Db	654	ACCAAGACAGCGCTGCGCGGCTGGCGCTTGTGCGAGTGCCTGCGCGCGG	713
QY	361	AAACCGCAACCTTCTTAGAGGACGTGCGAGAACTGGAGCTGGCGAGGAGGACCC	420
Db	714	AAACCGCAACCTTCTTAGAGGACGTGCGAGAACTGGAGCTGGCGAGGAGGACCC	773

QY 421 GAAGAGCGAGTGGCTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAGAG 480
Db 774 GAAGAGCGAGTGGCTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAGAG 833
QY 481 CAGCCCTTTAAGGATTTCTGACCAAGCGCTTCTACGACAAGTTTCTGCAAGTGAACATC 540
Db 834 CAGCCCTTTAAGGATTTCTGACCAAGCGCTTCTACGACAAGTTTCTGCAAGTGAACATC 893
QY 541 TTCGAGATGCAACCGAGTGTGACAGATGATCTTCACTGAGTGTGAGGAAAGGT 600
Db 894 TTCGAGATGCAACCGAGTGTGACAGATGATCTTCACTGAGTGTGAGGAAAGGT 953
QY 601 GGTTTTGGGAGGTATGTCCTCCAGGTGAACACACCTGCGAAGATGATGCTGCTGAG 660
Db 954 GGTTTTGGGAGGTATGTCCTCCAGGTGAACACACCTGCGAAGATGATGCTGCTGAG 1013
QY 661 AACTCGGACAAGCGGCTGAAGAAAGGTGCGAAGATGGCTCTCTTGGAAAG 720
Db 1014 AACTCGGACAAGCGGCTGAAGAAAGGTGCGAAGATGGCTCTCTTGGAAAG 1073
QY 721 GAAATCTTGGAGAAGTCAAGAGCCCTTTCATGTCTCTGCGCTATGCTTGGAGC 780
Db 1074 GAAATCTTGGAGAAGTCAAGAGCCCTTTCATGTCTCTGCGCTATGCTTGGAGC 1133
QY 781 AAGACCCATCTCTGCTTGTGATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC 840
Db 1134 AAGACCCATCTCTGCTTGTGATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC 1193
QY 841 TACACGTGGGACGCGTGGCTGACATGACCGGCTGATCTTTTACTCGGCCAGATA 900
Db 1194 TACACGTGGGACGCGTGGCTGACATGACCGGCTGATCTTTTACTCGGCCAGATA 1253
QY 901 GCCTGTGGATCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCTGAG 960
Db 1254 GCCTGTGGATCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCTGAG 1313
QY 961 AATGTCTTGGATGACCTCGGAACTGACAGTTATCTGACCTGGGGTGGCGTGGAG 1020
Db 1314 AATGTCTTGGATGACCTCGGAACTGACAGTTATCTGACCTGGGGTGGCGTGGAG 1373
QY 1021 ATGAGGTTGGCAAGCCATACCCAGAGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
Db 1374 ATGAGGTTGGCAAGCCATACCCAGAGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433
QY 1081 ATCTTAATGGAAGGTAAGTTATTTCTATCTGTGGACTGTTTGGCATGGGATGCAGC 1140
Db 1434 ATCTTAATGGAAGGTAAGTTATTTCTATCTGTGGACTGTTTGGCATGGGATGCAGC 1493
QY 1141 ATTTATGAAATGGTTGCTGGAGCAACACCATTTCAAAGATTACAAGAAAGGTCAATAA 1200
Db 1494 ATTTATGAAATGGTTGCTGGAGCAACACCATTTCAAAGATTACAAGAAAGGTCAATAA 1553
QY 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCGAGGTCAAATTCACAGCATGAATTTACA 1260
Db 1554 GAGGATCTGAAGCAAGAACTCTGCAAGCGAGGTCAAATTCACAGCATGAATTTACA 1613
QY 1261 GAGGAAGCAAAAGATATTTGCAAGGCTCTTCTGGCTAAAGAAACACAGCAAGCTTAGGA 1320
Db 1614 GAGGAAGCAAAAGATATTTGCAAGGCTCTTCTGGCTAAAGAAACACAGCAAGCTTAGGA 1673
QY 1321 AGCAGAAAAGTCTGATGATCCCAAGGAAACATCAATTTCTTTAAACGATCAACTTTCT 1380
Db 1674 AGCAGAAAAGTCTGATGATCCCAAGGAAACATCAATTTCTTTAAACGATCAACTTTCT 1733
QY 1381 CGCTGGAAGCTGGCTAATTAACCCCATTTGTCAGACCCCTTCAGTGGTTATGCC 1440
Db 1734 CGCTGGAAGCTGGCTAATTAACCCCATTTGTCAGACCCCTTCAGTGGTTATGCC 1793
QY 1441 AAGACATCGCTGAAATGATATTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1500
Db 1794 AAGACATCGCTGAAATGATATTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1853
QY 1501 GATAAGCAGTTCTTCAAAACATTTTCGACAGAGTGTCTTCTATAGCATGCGAGGAAG 1560

RESULT 3

US-09-802-117-1

; Sequence 1, Application US/09802117

; Patent No. 6444456

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wilganowski, Nathaniel L.

; TITLE OF INVENTION: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polyn

; FILE REFERENCE: LEX-0147-USA

; CURRENT APPLICATION NUMBER: US/09/802,117

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 60/188,449

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1662

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-802-117-1

Query Match 99.8%; Score 1655.4; DB 3; Length 1662;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTGGACATGGGGGCCCTCGACAACTGATCGCAACACCGCTACTCTGCAGGCCCGG 60
Db 1 ATGGTGGACATGGGGGCCCTCGAYAACCTGATCGCAACACCGCTACTCTGCAGGCCCGG 60
QY 61 AAGCCCTCGACTGCGACAGCAAAAGAGCTGCAGCGCGCGGCTAGCCTTGCCCTGCCC 120
Db 61 AAGCCCTCGACTGCGACAGCAAAAGAGCTGCAGCGCGCGGCTAGCCTTGCCCTGCCC 120
QY 121 GGGCTGACAGGCTGGCGGAGCTCGCCAGAAAGCTGTCCCTGAACCTTCCACAGCCTGTGT 180
Db 121 GGGCTGACAGGCTGGCGGAGCTCGCCAGAAAGCTGTCCCTGAACCTTCCACAGCCTGTGT 180
QY 181 GAGCAGCAGCCATCGGTGCGCGCTCTTCCTGACTTCTTAGCCACAGTGCACAGCTTC 240
Db 181 GAGCAGCAGCCATCGGTGCGCGCTCTTCCTGACTTCTTAGCCACAGTGCACAGCTTC 240
QY 241 CGCAAGCGGCAACCTTCTTAGAGACCTGTCAGAACTGGGAGCTGGCGAGGAGGACCC 300
Db 241 CGCAAGCGGCAACCTTCTTAGAGACCTGTCAGAACTGGGAGCTGGCGAGGAGGACCC 300
QY 301 ACCAAGACAGCGGCTGCGAGGGGTGTGGCCACTTGTGGAGTGCCTTGCCTCCCGGGG 360
Db 301 ACCAAGACAGCGGCTGCGAGGGGTGTGGCCACTTGTGGAGTGCCTTGCCTCCCGGGG 360
QY 361 AACCGCAACCTTCTTCAGCAGCGCTGCGCCACCAAGTGCAGAGCACCACCTGAG 420
Db 361 AACCGCAACCTTCTTCAGCAGCGCTGCGCCACCAAGTGCAGAGCACCACCTGAG 420
QY 421 GAAGAGCAGTGGCTGCAAGTGCAGCTGCGCAAGGCTGAGGCGCATGGCTTTCTTGAAGAG 480
Db 421 GAAGAGCAGTGGCTGCAAGTGCAGCTGCGCAAGGCTGAGGCGCATGGCTTTCTTGAAGAG 480
QY 481 CAGCCCTTAAGGATTTGCTGACAGCGCCTTCTACGACAAAGTTTCTGCAAGTGAACATC 540

Db 481 CAGCCCTTTAAGGATTTTCGTGACAGCGCCTTCTACGACAAAGTTTCTCGAGTGGAAACTC 540
Qy 541 TTCGAGATGCAACCAAGTGTGAGCAAGTATCTTCACTGAGTTTCAGAGTGTCTGGGAAAGGT 600
Db 541 TTCGAGATGCAACCAAGTGTGAGCAAGTATCTTCACTGAGTTTCAGAGTGTCTGGGAAAGGT 600
Qy 601 GGTTTTGGGAGGTATGTGCGGTGCGGTGAGGAGAAACACTGGGAAAGATGATGCTGTGAAG 660
Db 601 GGTTTTGGGAGGTATGTGCGGTGCGGTGAGGAGAAACACTGGGAAAGATGATGCTGTGAAG 660
Qy 661 AAATGGGACAAAGCGGCTGAGAAAGAAAGGTGGGAGAGATGGCTCTCTTGGAAAG 720
Db 661 AAATGGGACAAAGCGGCTGAGAAAGAAAGGTGGGAGAGATGGCTCTCTTGGAAAG 720
Qy 721 GAAATCTTGGAGAGGTGAGAGCGCTTTCATGTCTCTCTGCGCTATGCTTCTTGAGAGC 780
Db 721 GAAATCTTGGAGAGGTGAGAGCGCTTTCATGTCTCTCTGCGCTATGCTTCTTGAGAGC 780
Qy 781 AAGACCCATCTGCTGCTGATGAGCTGATGATGGGAGAGCTTCAAGTTTCCACATC 840
Db 781 AAGACCCATCTGCTGCTGATGAGCTGATGATGGGAGAGCTTCAAGTTTCCACATC 840
Qy 841 TACAACTGGGACAGCGGTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 900
Db 841 TACAACTGGGACAGCGGTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 900
Qy 901 GCTGTGGATGCTGCACTCATGAACTCGGCATCTGATCGGAGCATGAGCTTCTGAG 960
Db 901 GCTGTGGATGCTGCACTCATGAACTCGGCATCTGATCGGAGCATGAGCTTCTGAG 960
Qy 961 AATGTGCTTCTGATGACCTCGGCAACTGACGTTTATCTGACCTGGGCTGGCGTGGAG 1020
Db 961 AATGTGCTTCTGATGACCTCGGCAACTGACGTTTATCTGACCTGGGCTGGCGTGGAG 1020
Qy 1021 ATGAAGGTGGCAAGCCCATACCCAGAGGGTGGAAACCAATGGTTTACATGGCTCCTGAG 1080
Db 1021 ATGAAGGTGGCAAGCCCATACCCAGAGGGTGGAAACCAATGGTTTACATGGCTCCTGAG 1080
Qy 1081 ATCTTAATGGAAGTAAAGTTATTCCTATCTGTGGAGTGGTTTGGCCATGGAGTGCAGC 1140
Db 1081 ATCTTAATGGAAGTAAAGTTATTCCTATCTGTGGAGTGGTTTGGCCATGGAGTGCAGC 1140
Qy 1141 ATTTATGAATGGTTGCTGGAAGCAACCAATTCAGAGATTAACAAGAAAGGTTCAGTAA 1200
Db 1141 ATTTATGAATGGTTGCTGGAAGCAACCAATTCAGAGATTAACAAGAAAGGTTCAGTAA 1200
Qy 1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTCAAAATTCAGAGATTAACATTCACA 1260
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTCAAAATTCAGAGATTAACATTCACA 1260
Qy 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTGGCTTAAGAAACAGAGCAAGCTTAGGA 1320
Db 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTGGCTTAAGAAACAGAGCAAGCTTAGGA 1320
Qy 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTCT 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTCT 1380
Qy 1381 CGCTGGAAGTGGCTTAATGAAACCCCATTTTGGCCAGAGCGCTTCACTGTTTATGCC 1440
Db 1381 CGCTGGAAGTGGCTTAATGAAACCCCATTTTGGCCAGAGCGCTTCACTGTTTATGCC 1440
Qy 1441 AAGACATCGCTGAATATGATGATTTCTGAGTTTCGGGGTGGAAATTCATGACAAA 1500
Db 1441 AAGACATCGCTGAATATGATGATTTCTGAGTTTCGGGGTGGAAATTCATGACAAA 1500
Qy 1501 GATAAGCAGTTCTTCAAAAACCTTGGCAGAGGTGCTGTTTCTTATAGCATGGCAGGAGAA 1560
Db 1501 GATAAGCAGTTCTTCAAAAACCTTGGCAGAGGTGCTGTTTCTTATAGCATGGCAGGAGAA 1560
Qy 1561 ATTATAGAACGGGACTGTTTGGAGAACTGAAATGACCCCAACAGACTACGGGTGTGAG 1620
Db 1561 ATTATAGAACGGGACTGTTTGGAGAACTGAAATGACCCCAACAGACTACGGGTGTGAG 1620

Qy 1621 GAGGTAATTCATCCAGTCTGGGTGTGTTTGTATTG 1659
Db 1621 GAGGTAATTCATCCAGTCTGGGTGTGTTTGTATTG 1659

RESULT 4

US-10-217-745-1
; Sequence 1, Application US/10217745
; Patent No. 683275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 683275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT FILING DATE: 2002-08-12
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-1.

Query Match 99.8%; Score 1655.4; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGTGTGACATGGGGCCCTGGACAACTGATCCCAACACCGCTACCTGACGCGCGG 60
Db 1 ATGTGTGACATGGGGCCCTGGAYAACTGATGCCAACACCGCTACCTGACGCGCGG 60
Qy 61 AAGCCCTCGGACTCGGACAGCAAGAGCTGAGCGGGGGGGGGCTAGCTGGCCCTGCCC 120
Db 61 AAGCCCTCGGACTCGGACAGCAAGAGCTGAGCGGGGGGGGGCTAGCTGGCCCTGCCC 120
Qy 121 GGGTGTGAGGCTCGGCGGAGCTCGCCAGAGCTGCTCCCTGAACTTCCAGAGCTGTGT 180
Db 121 GGGTGTGAGGCTCGGCGGAGCTCGCCAGAGCTGCTCCCTGAACTTCCAGAGCTGTGT 180
Qy 181 GAGCAGCAGCCATCGGTCGCGCTCTTCCTGCTGACTTCTAGCCACAGTGCACAGTTC 240
Db 181 GAGCAGCAGCCATCGGTCGCGCTCTTCCTGCTGACTTCTAGCCACAGTGCACAGTTC 240
Qy 241 CGCAAGCGGCAACCTTCTTAGAGAGCTGAGAGAACTGGGAGCTGGCCGAGAGGAGCCC 300
Db 241 CGCAAGCGGCAACCTTCTTAGAGAGCTGAGAGAACTGGGAGCTGGCCGAGAGGAGCCC 300
Qy 301 ACCAAGACAGCGGCTCGAGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCCCCGGGG 360
Db 301 ACCAAGACAGCGGCTCGAGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCCCCGGGG 360
Qy 361 AACCCGCAACCTTCTCCTCAGCCAGCGCTGCGCCAAAGCTGAGGGCCATGGCTTCTTGAAGAG 480
Db 361 AACCCGCAACCTTCTCCTCAGCCAGCGCTGCGCCAAAGCTGAGGGCCATGGCTTCTTGAAGAG 480
Qy 421 GAAGAGCAGGTGGTGTGAGTGCAGCTGCGCAAGGCTGAGGGCATGGCTTCTTGAAGAG 480
Db 421 GAAGAGCAGGTGGTGTGAGTGCAGCTGCGCAAGGCTGAGGGCCATGGCTTCTTGAAGAG 480
Qy 481 CAGCCCTTTAAGGATTTCTGTGACAGCGCTTCTACGACAAAGTTTCTGAGTGGAACTC 540
Db 481 CAGCCCTTTAAGGATTTCTGTGACAGCGCTTCTGTACGACAAAGTTTCTGAGTGGAACTC 540
Qy 541 TTCGAGATGCAACCAAGTGTGAGCAAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGGT 600
Db 541 TTCGAGATGCAACCAAGTGTGAGCAAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGGT 600

601 GGTGTTGGGAGGATATGTCCTCAGGTGAAACACCTGGGAAGATGATGCTGTAAAG 660
601 GGTGTTGGGAGGATATGTCCTCAGGTGAAACACCTGGGAAGATGATGCTGTAAAG 660
661 AAACCTGGACAAGAGCGGCTGAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
661 AAACCTGGACAAGAGCGGCTGAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
721 GAAATCTTGGAGAAGGTGAGAGCCCTTTCAATGTCTCTGCGCCTATGCTTGGAGAGC 780
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781 AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGAGCTCAAGTTCCACATC 840
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1201 GAGGATCTGAAGCAAGAACTCTGACAGAGAGTCAAAATTCAGAGATTAACCTTACA 1260
1261 GAGGAAGCAAGAGATATTTGACAGGCTCTTCTTGGCTTAAGAAACCAAGAGTAACT 1320
1261 GAGGAAGCAAGAGATATTTGACAGGCTCTTCTTGGCTTAAGAAACCAAGAGTAACT 1320
1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTCT 1380
1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTCT 1380
1381 GCGCTGGAAGCTGGCTTAATGAACCCCATTTGTCGACAGCCCTTCAAGTGTATGTC 1440
1381 GCGCTGGAAGCTGGCTTAATGAACCCCATTTGTCGACAGCCCTTCAAGTGTATGTC 1440
1441 AAGACATGCTGAAATGATCAATTTCTGAGGTTGGGGGTGGAAATTCATGACAAA 1500
1441 AAGACATGCTGAAATGATCAATTTCTGAGGTTGGGGGTGGAAATTCATGACAAA 1500
1501 GATAAGCAGTCTCTCAAAAATTTGCGACAGGTGCTGTTCTTATAGCATGGCAGGAAG 1560
1501 GATAAGCAGTCTCTCAAAAATTTGCGACAGGTGCTGTTCTTATAGCATGGCAGGAAG 1560
1561 ATTATAGAAACGGGACTGTTGAGGAACTGAATGACCCCAACAGACCTACGGGTGTGAG 1620
1561 ATTATAGAAACGGGACTGTTGAGGAACTGAATGACCCCAACAGACCTACGGGTGTGAG 1620
1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659
1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 5
US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-738-894A-1

Query Match 99.7%; Score 1654.2; DB 3; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTTGGAATGATGGGGCCCTGGACAACTGATCGCAACACCGCTTACTGTCAGGCCCGG 60
DB 1 ATGTTGGAATGATGGGGCCCTGGACAACTGATCGCAACACCGCTTACTGTCAGGCCCGG 60
QY 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCGAGCGGCGGCGGTAGCTGSCCTGCC 120
DB 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCGAGCGGCGGCGGTAGCTGSCCTGCC 120
QY 121 GGGCTGACAGGCTGCGCGGAGCTCGCGCAGAGCTGCTCCCTGAACTTCCACAGCTGTGT 180
DB 121 GGGCTGACAGGCTGCGCGGAGCTCGCGCAGAGCTGCTCCCTGAACTTCCACAGCTGTGT 180
QY 181 GAGCAGCAGCCATCGGTGCGGCTCTTCCGTGACTTCTTAGCCACAGTGCCTGCTTCC 240
DB 181 GAGCAGCAGCCATCGGTGCGGCTCTTCCGTGACTTCTTAGCCACAGTGCCTGCTTCC 240
QY 241 CGCAAGCGGCAACCTTCTTAGAGACCTGCGAGAACTGGGAGCTGGCGAGGAGGACCC 300
DB 241 CGCAAGCGGCAACCTTCTTAGAGACCTGCGAGAACTGGGAGCTGGCGAGGAGGACCC 300
QY 301 ACCAAGACAGCGGCTGCGAGGCTGCTGCGGCTTCTGAGGCTGCGGAGGAGGAGCC 360
DB 301 ACCAAGACAGCGGCTGCGAGGCTGCTGCGGCTTCTGAGGCTGCGGAGGAGGAGCC 360
QY 361 AACCCGCAACCTTCTTAGAGACCTGCGAGAACTGGGAGCTGGCGAGGAGGAGCC 420
DB 361 AACCCGCAACCTTCTTAGAGACCTGCGAGAACTGGGAGCTGGCGAGGAGGAGCC 420
QY 421 GAAGGCGAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCTTCTTCTGCAAGAG 480
DB 421 GAAGGCGAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCTTCTTCTGCAAGAG 480
QY 481 CAGCCCTTTAAGGATTTCTGACAGCGGCTTCTAGCAAGTCTTCTGAGTGGAACTC 540
DB 481 CAGCCCTTTAAGGATTTCTGACAGCGGCTTCTAGCAAGTCTTCTGAGTGGAACTC 540
QY 541 TTCCGAGATGCAACCAAGTGTGACAAAGTACTTCTAGTTCAGAGTTCAGAGTTCAG 600
DB 541 TTCCGAGATGCAACCAAGTGTGACAAAGTACTTCTAGTTCAGAGTTCAGAGTTCAG 600
QY 601 GGTGTTGGGAGGATGATGTCCTGAGTGAAGAACTGGGAAGATGATGCTGTGTAAG 660
DB 601 GGTGTTGGGAGGATGATGTCCTGAGTGAAGAACTGGGAAGATGATGCTGTGTAAG 660
QY 661 AAACTGGACAGAGCGGCTGAGAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
DB 661 AAACTGGACAGAGCGGCTGAGAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 720

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QY 721 GAAATCTTGGAGAGAGTGCAGAGCCCTTTTCTCTCTGCGCTATGCTTGCCTTTGAGAGC 780
Db 721 GAAATCTTGGAGAGAGTGCAGAGCCCTTTTCTCTCTGCGCTATGCTTGCCTTTGAGAGC 780
QY 781 AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGAGAGCTCAAGTTCACATC 840
Db 781 AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGAGAGCTCAAGTTCACATC 840
QY 841 TACAACTGGGCAACGCTGGCTGACATGAGCCGGGTGATCTTTTACTCGGCCCCAGATA 900
Db 841 TACAACTGGGCAACGCTGGCTGACATGAGCCGGGTGATCTTTTACTCGGCCCCAGATA 900
QY 901 GCCTGGAGTCTGCACCTCATGAACTGCGCATCTGCTATGCGGACATGAAGCCTGAG 960
Db 901 GCCTGGAGTCTGCACCTCATGAACTGCGCATCTGCTATGCGGACATGAAGCCTGAG 960
QY 961 AATGTGCTTCTGGATGACTCGGCAACTGACAGTTTATCTGACCTGGGCTGGCGTGGAG 1020
Db 961 AATGTGCTTCTGGATGACTCGGCAACTGACAGTTTATCTGACCTGGGCTGGCGTGGAG 1020
QY 1021 ATGAAGGCTGGCAAGCCCATACCCAGAGGCTGGAAACCAATGGTTACATGGCTCCTGAG 1080
Db 1021 ATGAAGGCTGGCAAGCCCATACCCAGAGGCTGGAAACCAATGGTTACATGGCTCCTGAG 1080
QY 1081 ATCTTAATGGAAAGGTAACTTATCTCTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1140
Db 1081 ATCTTAATGGAAAGGTAACTTATCTCTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1140
QY 1141 ATTTATGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1200
Db 1141 ATTTATGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1200
QY 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCACGATGATACTTCA 1260
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCACGATGATACTTCA 1260
QY 1261 GAGGAGCAAAAGATATTTGAGGCTTCTTGGCTTAAGAAACCAAGACGCTTTAGGA 1320
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QY 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCACTTTCT 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCACTTTCT 1380
QY 1381 CCGCTGGAAGCTGGCTTAATTAAGCCCAATTTGCGCAGACCTTCACTGCTTTATGCC 1440
Db 1381 CCGCTGGAAGCTGGCTTAATTAAGCCCAATTTGCGCAGACCTTCACTGCTTTATGCC 1440
QY 1441 AAAGACATCGCTGAAATGATGATTTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA 1500
Db 1441 AAAGACATCGCTGAAATGATGATTTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA 1500
QY 1501 GATAAGCAGTTCTTCAAAACTTTTCGACAGTGTCTTCTATAGCATGCGAGAGAA 1560
Db 1501 GATAAGCAGTTCTTCAAAACTTTTCGACAGTGTCTTCTATAGCATGCGAGAGAA 1560
QY 1561 ATTATAGAAACGGGACTGTTGAGGAATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 ATTATAGAAACGGGACTGTTGAGGAATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTTATTG 1659
Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTTATTG 1659
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RESULT 6
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/739,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1

Query Match 99.7%; Score 1654.2; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGTGGACATGGGGGCGCTCGACAACTGATCGCAACACCGCTACTCTGCAGGCCGG 60
Db 1 ATGTGGACATGGGGGCGCTCGACAACTGATCGCAACACCGCTACTCTGCAGGCCGG 60
QY 61 AAGCCCTCGACTCGACAGCAAAAGAGCTGAGCGGCGGGCTAGCTGGCCCTGCC 120
Db 61 AAGCCCTCGACTCGACAGCAAAAGAGCTGAGCGGCGGGCTAGCTGGCCCTGCC 120
QY 121 GGGCTGACGGGCTCGCGGAGCTCGCAGAGAGCTGCTCCGAACTTCCACAGCCCTGT 180
Db 121 GGGCTGACGGGCTCGCGGAGCTCGCAGAGAGCTGCTCCGAACTTCCACAGCCCTGT 180
QY 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACGTT 240
Db 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACGTT 240
QY 241 CGCAAGCGGCAACCTTCTTAGAGAGCTGAGAGAACTGGGAGCTGGCGGAGGAGCC 300
Db 241 CGCAAGCGGCAACCTTCTTAGAGAGCTGAGAGAACTGGGAGCTGGCGGAGGAGCC 300
QY 301 ACCAAGACAGCGGCTGCGGAGCTGCGGCTGCTGAGTGGCGGCTGCGGCTGCGGCGG 360
Db 301 ACCAAGACAGCGGCTGCGGAGCTGCGGCTGCTGAGTGGCGGCTGCGGCTGCGGCGG 360
QY 361 AACCCGCAACCTTCTCAGCAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 420
Db 361 AACCCGCAACCTTCTCAGCAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 420
QY 421 GAAAGCAGTGGCTGAGTGAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
Db 421 GAAAGCAGTGGCTGAGTGAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
QY 481 CAGCCCTTAAAGGATTTGTCAGCAGCGGCTTCTACGACAAAGTTTCTGAGTGGAACTC 540
Db 481 CAGCCCTTAAAGGATTTGTCAGCAGCGGCTTCTACGACAAAGTTTCTGAGTGGAACTC 540
QY 541 TTCAGATGCAACCAAGTGTGAGCAAGTACTTCACTAGTTCAGAGTCTGGGAAAGGT 600
Db 541 TTCAGATGCAACCAAGTGTGAGCAAGTACTTCACTAGTTCAGAGTCTGGGAAAGGT 600
QY 601 GGTGTTGGGAGGATGTCGCTGAGTGAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 660
Db 601 GGTGTTGGGAGGATGTCGCTGAGTGAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 660
QY 661 AAATGGAAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 720
Db 661 AAATGGAAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 720
QY 721 GAAATCTTGGAGAGGCTGAGGCTTCTTCTGCTCTCTGCGCTATGCTTGTGAGAGC 780
Db 721 GAAATCTTGGAGAGGCTGAGGCTTCTTCTGCTCTCTGCGCTATGCTTGTGAGAGC 780
QY 781 AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGAGAGCTCAAGTTCACATC 840

781 AAGACCCATCTCTGCTTGTGATGAGCTGATGAATGGGGAGAGCTCAAGTTCCACATC 840
841 TACAACTGGGCACTGGGCTTGGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 900
841 TACAACTGGGCACTGGGCTTGGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 900
901 GCCTGTGGATGCTGACCTCATGAATCTGGCATCTGCTATCGGGACATGAAGCTGAG 960
901 GCCTGTGGATGCTGACCTCATGAATCTGGCATCTGCTATCGGGACATGAAGCTGAG 960
961 AATGCTCTCTGATGAGCTCGGCACTGCAAGCTTATCTGACCTGGGCTGGCCGTGAG 1020
961 AATGCTCTCTGATGAGCTCGGCACTGCAAGCTTATCTGACCTGGGCTGGCCGTGAG 1020
1021 ATGAAGGGTGGCAAGCCCATCAACCCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG 1080
1021 ATGAAGGGTGGCAAGCCCATCAACCCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG 1080
1081 ATCTTAATGGAAGAGTAAATTTATCTTATCTGAGCTGCTTATCGGCTGGCCGTGAG 1140
1081 ATCTTAATGGAAGAGTAAATTTATCTTATCTGAGCTGCTTATCGGCTGGCCGTGAG 1140
1141 ATTTATGAATGCTGCTGGACGACCAATTCAGATTAAGATTCAAGGAAGAGTCAATAA 1200
1141 ATTTATGAATGCTGCTGGACGACCAATTCAGATTAAGATTCAAGGAAGAGTCAATAA 1200
1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGTCAAAATTCAGCATGATTAATTCACA 1260
1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGTCAAAATTCAGCATGATTAATTCACA 1260
1261 GAGGAAGCAAGAACTCTGCAAGACGAGTCAAAATTCAGCATGATTAATTCACA 1320
1261 GAGGAAGCAAGAACTCTGCAAGACGAGTCAAAATTCAGCATGATTAATTCACA 1320
1321 AGCAGAGAAAGTCTGATGATCCCAAGGAAACATCAATTTCTTAAACGATCACTTCTT 1380
1321 AGCAGAGAAAGTCTGATGATCCCAAGGAAACATCAATTTCTTAAACGATCACTTCTT 1380
1381 CGCTGGAAGCTGGCTTAATTAAGCCCATTTGTCAGACGCTTCAAGTGGTTTATGCC 1440
1381 CGCTGGAAGCTGGCTTAATTAAGCCCATTTGTCAGACGCTTCAAGTGGTTTATGCC 1440
1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1500
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1501 GATAGCAGTCTTCAAAAACCTTTGCGACAGTGTCTTCTATAGCATGGCAGGAAGA 1560
1561 ATTATAGAAACGGGACTGTTTGGAGAACTGATGATGACCCCAAGACCTACGGTTTGTAG 1620
1561 ATTATAGAAACGGGACTGTTTGGAGAACTGATGATGACCCCAAGACCTACGGTTTGTAG 1620
1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659
1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 7
US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3
Query Match 63.1%; Score 1046.8; DB 3; Length 1062;
Best Local Similarity 99.8%; Pred. No. 5.8e-259; Indels 0; Gaps 0;
Matches 1048; Conservative 0; Mismatches 2;
QY 1 ATGTGGAGATGGGGGCTTGGACAACTGATCGCAACACACCGCTTACCTGAGGCGCCG 60
Db 1 ATGTGGAGATGGGGGCTTGGACAACTGATCGCAACACACCGCTTACCTGAGGCGCCG 60
QY 61 AAGCCCTCGGATGCGGACGAGCTGAGCGGCGGCGGCTAGCCTGCGCCCTGCCC 120
Db 61 AAGCCCTCGGATGCGGACGAGCTGAGCGGCGGCGGCTAGCCTGCGCCCTGCCC 120
QY 121 GGGCTGCAAGGCTGCGGAGCTCGCCAGAGCTGCTGAACTTCCACAGCTGTGT 180
Db 121 GGGCTGCAAGGCTGCGGAGCTCGCCAGAGCTGTCTTGAATTTCCACAGCTGTGT 180
QY 181 GAGCAGACGCTTCTGCGCGCTTCTTCTGAGCTTCTAGCCACAGTGCCTGCTT 240
Db 181 GAGCAGACGCTTCTGCGCGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCTT 240
QY 241 CGCAAGCGGCAACCTTCTGAGGACCTGCGGAGCTGCGGAGCTGCGGAGGAGGACCC 300
Db 241 CGCAAGCGGCAACCTTCTGAGGACCTGCGGAGCTGCGGAGCTGCGGAGGAGGACCC 300
QY 301 ACCAAGACAGCGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGGAGGAGGACCC 360
Db 301 ACCAAGACAGCGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGGAGGAGGACCC 360
QY 361 AACCGCAACCTTCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGGAGGAGGACCC 420
Db 361 AACCGCAACCTTCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGGAGGAGGACCC 420
QY 421 GAAAGCAGTGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGGAGGAGGAGGACCC 480
Db 421 GAAAGCAGTGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGGAGGAGGAGGACCC 480
QY 481 CAGCCCTTAAAGGATTTCTGAGCAGCTGCTTACGACAGCTTCTGAGTGGGAACTC 540
Db 481 CAGCCCTTAAAGGATTTCTGAGCAGCTGCTTACGACAGCTTCTGAGTGGGAACTC 540
QY 541 TTCGAGATGCAACCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGT 600
Db 541 TTCGAGATGCAACCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGT 600
QY 601 GGTGTTGGGAGGATGTCCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 601 GGTGTTGGGAGGATGTCCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 AAATGGAACAGAGCGGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 661 AAATGGAACAGAGCGGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 GAAATCTTGGAGAGGCTCAGCAGGCTTCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAG 780
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QY 781 AAGACCCATCTCTGCTTGTATGAGCTGATGAATGGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 781 AAGACCCATCTCTGCTTGTATGAGCTGATGAATGGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 TACAACGTGGGACGCGTGGCTGAGCATGAGCGGCTGATCTTTTACTCGGCCAGATA 900
Db 841 TACAACGTGGGACGCGTGGCTGAGCATGAGCGGCTGATCTTTTACTCGGCCAGATA 900

QY 901 GCCTGTGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGACATGAAGCCTGAG 960
Db 901 GCCTGTGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGACATGAAGCCTGAG 960
QY 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGCTGGCGTGGAG 1020
Db 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGCTGGCGTGGAG 1020
QY 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGG 1050
Db 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGG 1050

RESULT 8

US-10-217-745-3
; Sequence 3, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-3

Query Match 63.1%; Score 1046.8; DB 4; Length 1062;
Best Local Similarity 99.8%; Pred. No. 5.8e-259;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGGGATGCGGCGCCCTGACAACTGATCGCAACACCGCCCTACTGCGAGCCCGG 60
Db 1 ATGTGGGATGCGGCGCCCTGACAACTGATCGCAACACCGCCCTACTGCGAGCCCGG 60
QY 61 AAGCCCTCGACTGCGACAGCAAGAGCTGCAAGCGCGCGGCGTAGCCTGCGCCCTGCC 120
Db 61 AAGCCCTCGACTGCGACAGCAAGAGCTGCAAGCGCGCGGCGTAGCCTGCGCCCTGCC 120
QY 121 GGGCTGCAAGGCTGCGCGGAGCTCCGCAAGAGCTGCTCCAACTTCCACAGCCTGTGT 180
Db 121 GGGCTGCAAGGCTGCGCGGAGCTCCGCAAGAGCTGCTCCAACTTCCACAGCCTGTGT 180
QY 181 GAGCAGCAGCCCATCGGTCGCGCCCTCTTCCTGAGCTTCTAGCCACAGTGCACAGTTC 240
Db 181 GAGCAGCAGCCCATCGGTCGCGCCCTCTTCCTGAGCTTCTAGCCACAGTGCACAGTTC 240
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Db 301 ACCAAGACAGCGCTGCGAGGCTGCGGCACTTGTGCGAGTGCCTCCCGCGGG 360
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QY 481 CAGCCCTTTAAGGATTTCTGTGACCGCGCCTTCTACGACAAGTTTCTGCACTGGAAATC 540
Db 481 CAGCCCTTTAAGGATTTCTGTGACCGCGCCTTCTACGACAAGTTTCTGCACTGGAAATC 540
QY 541 TTCGAGATGCAACAGAGTGTGAGCAAGTACTTCACTAGTTTCAAGTGTGCGGAAAGGT 600
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Db 721 GAAATCTTGGAGAGGTGACAGCCCTTTTCACTGCTCTCTGGCTATGCTTGGAGAGC 780
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Db 841 TACAACGTGGGACGCGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 901 GCCTGTGGATGCTGACACTCCATGAACTCGGCACTGCTATCGGACATGAAGCCTGAG 960
Db 901 GCCTGTGGATGCTGACACTCCATGAACTCGGCACTGCTATCGGACATGAAGCCTGAG 960
QY 961 AATGTGCTTCTGGATGACCTCGCAACTGCAAGTTATCTGACCTGGGCTGGCGTGGAG 1020
Db 961 AATGTGCTTCTGGATGACCTCGCAACTGCAAGTTATCTGACCTGGGCTGGCGTGGAG 1020
QY 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGG 1050
Db 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGG 1050

RESULT 9

US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

Query Match 37.2%; Score 617.4; DB 3; Length 36651;
Best Local Similarity 96.8%; Pred. No. 6.6e-148;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGTGGGATGCGGCGCCCTGACAACTGATCGCAACACCGCCCTACTGCGAGGCCCGG 60
Db 2076 ATGTGGGATGCGGCGCCCTGACAACTGATCGCAACACCGCCCTACTGCGAGGCCCGG 2135

QY 61 AAGCCCTCGGACTGCGAGCAGCAAGAGAGTGCAGCGCGCGCGCTAGCCTGCCCC 120
DB 2136 AAGCCCTCGGACTGCGAGCAGCAAGAGAGTGCAGCGCGCGCGCTAGCCTGCCCC 2195
QY 121 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGAGTGCCTGAACTTCCACAGCCTGTGT 180
DB 2196 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGAGTGCCTGAACTTCCACAGCCTGTGT 2255
QY 181 GAGCAGCAGCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 240
DB 2256 GAGCAGCAGCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 2315
QY 241 CGCAAGGCGGCAACCTTCTTAGAGAGAGTGCAGAACTGGAGCTGGCGAGGAGGCC 300
DB 2316 CGCAAGGCGGCAACCTTCTTAGAGAGAGTGCAGAACTGGAGCTGGCGAGGAGGCC 2375
QY 301 ACCAAGACAGCGCGCTCGAGGGCTGGTGGCACTTGTGGAGTGGCCCCGGGG 360
DB 2376 ACCAAGACAGCGCGCTCGAGGGCTGGTGGCACTTGTGGAGTGGCCCCGGGG 2435
QY 361 AACC CGCAACCTTCTCAGCAGCGCGCTGGCCACCAAGTGCCAGCAGCCACACTGAG 420
DB 2436 AACC CGCAACCTTCTCAGCAGCGCGCTGGCCACCAAGTGCCAGCAGCCACACTGAG 2495
QY 421 GAAGAGCAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 480
DB 2496 GAAGAGCAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 2555
QY 481 CAGCCCTTAAAGGATTTGTCAGCAGCGCTTCTACGACAAGTTCAGCAAGTTCAGTGGGAAAGGT 540
DB 2556 CAGCCCTTAAAGGATTTGTCAGCAGCGCTTCTACGACAAGTTCAGCAAGTTCAGTGGGAAAGGT 2615
QY 541 TTCGAGATGCAACCAAGTGCAGCAAGTTCCTAGTGGTTCAGAGTTCAGTGGGAAAGGT 600
DB 2616 TTCGAGATGCAACCAAGTGCAGCAAGTTCCTAGTGGTTCAGAGTTCAGTGGGAAAGGT 2675
QY 601 GGTTTGGGAGGTATGTGCGCTCAGGTGAAAACACTGGGAAGATGTAT 651
DB 2676 GGTTTGGGAGGTAAAGTGTCTCCAGTAGCCAGGCTAGAAAGGTGAAGCAT 2726

RESULT 10

US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THERIOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G

Query Match 37.2%; Score 617.4; DB 4; Length 36651;
Best Local Similarity 96.8%; Pred. No. 6.6e-148;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGTTGGACATGGGGGGCTTGACCAACCTGATCGCCAAACACCGCTACCTGACGGCCCGG 60
DB 2076 ATGTTGGACATGGGGGGCTTGACCAACCTGATCGCCAAACACCGCTACCTGACGGCCCGG 2135
QY 61 AAGCCCTCGGACTGCGAGCAGCAAGAGAGTGCAGCGCGCGCGCTAGCCTGCCCC 120
DB 2136 AAGCCCTCGGACTGCGAGCAGCAAGAGAGTGCAGCGCGCGCGCTAGCCTGCCCC 2195
QY 121 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGAGTGCCTGAACTTCCACAGCCTGTGT 180
DB 2196 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGAGTGCCTGAACTTCCACAGCCTGTGT 2255
QY 181 GAGCAGCAGCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 240
DB 2256 GAGCAGCAGCCATCGGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 2315
QY 241 CGCAAGGCGGCAACCTTCTTAGAGAGAGTGCAGAACTGGAGCTGGCGAGGAGGCC 300
DB 2316 CGCAAGGCGGCAACCTTCTTAGAGAGAGTGCAGAACTGGAGCTGGCGAGGAGGCC 2375
QY 301 ACCAAGACAGCGCGCTCGAGGGCTGGTGGCACTTGTGGAGTGGCCCCGGGG 360
DB 2376 ACCAAGACAGCGCGCTCGAGGGCTGGTGGCACTTGTGGAGTGGCCCCGGGG 2435
QY 361 AACC CGCAACCTTCTCAGCAGCGCGCTGGCCACCAAGTGCCAGCAGCCACACTGAG 420
DB 2436 AACC CGCAACCTTCTCAGCAGCGCGCTGGCCACCAAGTGCCAGCAGCCACACTGAG 2495
QY 421 GAAGAGCAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 480
DB 2496 GAAGAGCAGTGGCTGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 2555
QY 481 CAGCCCTTAAAGGATTTGTCAGCAGCGCTTCTACGACAAGTTCAGCAAGTTCAGTGGGAAAGGT 540
DB 2556 CAGCCCTTAAAGGATTTGTCAGCAGCGCTTCTACGACAAGTTCAGCAAGTTCAGTGGGAAAGGT 2615
QY 541 TTCGAGATGCAACCAAGTGCAGCAAGTTCCTAGTGGTTCAGAGTTCAGTGGGAAAGGT 600
DB 2616 TTCGAGATGCAACCAAGTGCAGCAAGTTCCTAGTGGTTCAGAGTTCAGTGGGAAAGGT 2675
QY 601 GGTTTGGGAGGTATGTGCGCTCAGGTGAAAACACTGGGAAGATGTAT 651
DB 2676 GGTTTGGGAGGTAAAGTGTCTCCAGTAGCCAGGCTAGAAAGGTGAAGCAT 2726

RESULT 11

US-08-464-954A-2
; Sequence 2, Application US/08464954A
; Patent No. 6255069
; GENERAL INFORMATION:
; APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,
; APPLICANT: PRIYA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR
; NUMBER OF INVENTION: KINASES GRK5 AND GRK6
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,954A
; FILING DATE: Herewith

:	CLASSIFICATION:	435			
:	PRIOR APPLICATION NUMBER:	08/076,084			
:	FILING DATE:	June 11, 1993			
:	ATTORNEY/AGENT INFORMATION:				
:	NAME:	Jane Massey Licata			
:	REGISTRATION NUMBER:	32,257			
:	REFERENCE/DOCKET NUMBER:	JEFF-0118			
:	TELECOMMUNICATION INFORMATION:				
:	TELEPHONE:	(609) 779-2400			
:	TELEFAX:	(609) 779-8488			
:	INFORMATION FOR SEQ ID NO:	2:			
:	SEQUENCE CHARACTERISTICS:				
:	LENGTH:	2848			
:	TYPE:	NUCLEIC ACID			
:	STRANDEDNESS:	SINGLE			
:	TOPOLOGY:	LINEAR			
:	ANTI-SENSE:	NO			
:	US-08-464-954A-2				
	Query Match	25.3%;	Score 419.8;	DB 3;	Length 2848;
	Best Local Similarity	56.2%;	Pred. No. 1.3e-97;		
	Matches	891;	Conservative	0;	Mismatches 682; Indels 12; Gaps 5
QY	15	GGCCTTGGCAACACTGATGCCAACACACCGCCTACTCTCACAGCCCGGAGCCCTTCGGAGTG	74		
Db	65	CGAGCTCGAGAACAATCGTAGCGAAACACGGTGCTACTCAAGGCCCGGAGGTGGCGGTGG	124		
QY	75	CGACAGCAANG---AGCTGCGAGCGCGCGCGGTAGCTTGGCCCTTGCCTGGGCTGCAGG	131		
Db	125	AATCGCAAAGGCNAAGAAATGGCGCAGATGCTCCAGTTCCCTCATCATGACCA	184		
QY	132	CTGCGCGGAGCTCCGCCAAGAAGCTGTCCCTGAACCTTCCACAGCCTGTGTGAGCAGCAGCC	191		
Db	185	GTGCGAAGACTGCGGCTCAGCCTCGACGCTGACTATCAGAGCTGTGCGAGCGGCACGC	244		
QY	192	CATCGGTGCGCGCCTCTTCCGTGACTTCTTAGCCACAGTGCCCACTGTCGGAAGCGCG	251		
Db	245	CATTGGGCGCTGTCTTCCGAGAGTTCTGTGCCACAGAGCCGGAGCTGAGCGCGTGCCT	304		
QY	252	AACCTTCTTAGAGCAGTGCAGAACTGGGAGCTGGCCGAGAGGGGACCACCAAGACAG	311		
Db	305	CGCCTTCTTGGATGGGGTGGCGAGTATGAAGTACCCCGGATGACAAAGCGAAGGCATG	364		
QY	312	CGCGCTGACAGGGGCTGGTGGCCACTTGTGCGAGTGGCCCTTGCCTCCCGGGAAACCCGCAACC	371		
Db	365	TGGGCGGCAGG---TAACGCGAATTTTCTGAGCCAACAGGCTCTGACCTCATCTCCCTGA	421		
QY	372	CTTCTCTACCCAGCGCGTGGCCACCAAGTGCACAGCAGCCACCACTGAGGAAGAGCGAGT	431		
Db	422	GGTCCCCCGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTTGCACAA	480		
QY	432	GGCTGAGTGACGCTGCCCAAGGCTGAGGCCATGGCTTTTCTTGCAAGAGCAGCCCTTAA	491		
Db	481	AGCTTTTCCAGGAATCTACCCGGCTGA--CCCACAGTACTCTGAGGCTGGCCCTTTTTC	538		
QY	492	GGATTTCTGACACCGGCTTCTACGACAGTTTCTGCACTGGAACCTCTTCGAGATGCA	551		
Db	539	CGACTACTCTGACAGCATCTACTTCAACCGTTTCTTGCAGTGAAGTGGCTGGAAAGGCA	598		
QY	552	ACCAGTGTGACAGAAGTACTTCACTGAGTTCTCAGAGTCTGGGGAAGGTGTTTTGGGA	611		
Db	599	GCCAGTGACAAAACACCTTCAGGCAATACCGAGTCTTGGGCAAGGTGGCTTTGGGA	658		
QY	612	GGTATGTGCGCTCGAGGTGAAAAACACTGGGAGATGATGCTGTGAAAGAACTGACAA	671		
Db	659	GGTGTGCGCTGCCCAAGTGGCGGCCACAGGTAAAGTATGATGCTCTCAAGAAAGCTAGAA	718		
QY	672	GAAAGCGGCTGAGAGAAAGGTGGCGAGAGATGGCTCTTCTGGAAAAGGAATCTTGA	731		
Db	719	AAGCGGATCAAGAAAGCGGAAGGGAGGCCATGGCGCTGAACGAGAAAGCATCTCTGA	778		
QY	732	GAAAGTGCAGAGCCCTTTTCATTGTCTCTCTGGCCCTATGCTTGTGAGCAAGACCATCT	791		

; ADDRESS: Botun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/221,817
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/123,932
 ; FILING DATE: 17 SEP 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 553215land, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31981
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2204 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 31..1758
 ; US-08-221-817-12

Query Match 25.2%; Score 418.2; DB 1; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 2.9e-97;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

Qy	15	GGCCCTGACAACTGATGCGCAACACCGCCTACTGACGCGCCGGAAGCCCTCGGACTG	74
Db	33	GGAGCTCGAAGACATCGTAGCAACACCGTGCTACTCAAGGCCCGGAAGGTGGCGTGG	92
Qy	75	CGACAGCAAG---AGCTGCAGCGCGCGCGGTAGCTGGCCCTGCCCGGCTCGAGG	131
Db	93	AAATCGCAAGGCCAAAGCAAGAAATGGCGGAGATGCTCCAGTTCCCTCACATCAGCCA	152
Qy	132	CTGCGCGGAGCTCCGCGCAAGCTGCTCCTGAACTTCCACAGCCTGTGTGACGACGAGCC	191
Db	153	GTGCGAAGAGTGGCGGCTCAGCTCGAGGTGACTATCACGCTGTGTGGAGCGGACGG	212
Qy	192	CATCGGTCCCGCCTCTTCCTCGTGAATCTAGCCACAGTGCCACGTTCCCGCAAGCGCGC	251
Db	213	CATTGGCGCCTGCTGTTCCGAGAGTCTGTGCCACGAGCGCGAGCTGAGCGCTGGCT	272
Qy	252	AACCTTCTAGAGAGCTGCAGAACTGGGAGCTGCGCGAGGAGGACCCACCAAGACAG	311
Db	273	CGCCTTCTGGATGGGTGGCGAGTATGAAGTGACCCCGGATGCAAGCGGAAGGCATG	332
Qy	312	CGCGCTGAGGGGCTGGTGGCCACTTGTGCGAGTGCCTCGCCCGCGGGAACCCGCAACC	371
Db	333	TGGGCGGACG---TAACGCAAGATTTCTGAGCCACAGGGTCTGACCTCATCCTTGA	389
Qy	372	CTTCTCAGCCAGCGCGTGGCCACCAAGTGCCAAGCAGCACCACTCAGGAGAGAGCGAGT	431
Db	390	GGTCCCGCGAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGCTCCCTCGAAAG	448
Qy	432	GGCTCAGTGACGCTGCGCAAGGCTGAGCCATGCGTTCTTTGGAAGAGCAGCCCTTTAA	491
Db	449	ACCTTTCCAGGAATCAACCGGCTGA---CCACAGTAGTACCTGAGCGTGGCCCTTTTGC	506

Qy	492	GGATTTCTGACCAAGCGCCTTCTAGCAACAAGTTTCTGCAAGTGAACATCTTTCGAGATGA	551
Db	507	CGACTACCTCGACAGCATCTACTTCAACCGTTTCTGCAAGTGAAGTGGCTGGAAGGCA	566
Qy	552	ACCAGTGTGACAGCAAGTACTTCACTGAGTCTCAGAGTGTGGGGAAGTGGTTTGGGGA	611
Db	567	GCCAGTGACCAAAACACCTTCAGGCAATACCGAGTCTTGGGTAAGGTGGCTTTGGGGA	626
Qy	612	GATATGTCCTCCAGGTGAAGAAACACCTGGGAAGATGTATGCTCTGAAGAACTGACAA	671
Db	627	GGTGTGCGCTGCCAGGTGCGGGCCACAGGTAAAGATGTATGCTCTGCAAGACCTAGAA	686
Qy	672	GAGCGGTGAAGAAAGGTGGCGAAGATGCTCTTTGGAAAAAGAAATCTTGA	731
Db	687	AAAGCGGATCAAGAAAGCGGAAGGCGGAGCCATGGCGCTGAACGAGAAGCAGATCCTGA	746
Qy	732	GAAGTGTGAGCGCCTTTCATTTGTTCTCTCGCCCTATGCTTGTGAGCAAGACCATCT	791
Db	747	GAAGTGAACAGTAGTGGTTGTAGTAGCTTGGCCCTACGCCCTATGAGCAAGGACGCGCT	806
Qy	792	CTGCCCTTGTATGAGCCTGATGAATGGGGGAGACCTCAAGTTTCCACATCTACAAGTGG	851
Db	807	GTGCTGTGTGACACTGATGAACGGGGGCGACCTCAAGTTTCCACATCTACCAATGG	866
Qy	852	CACGCTGGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAAGATAGCCTGTGGAT	911
Db	867	CCAGGCTGGCTTCCCGAAGCGCGGCGCTCTTCTACGCGCGGAGATCTGCTGTGGCCT	926
Qy	912	GCTGCACCTCATGAACTCGGCATGCTATCGGGACATGAAGCTGAGATGTGCTTCT	971
Db	927	GGAGGACCTGCACCGGGAGCGCATGCTGACAGGACCTGAAGGCCGAGAACATCTTGCT	986
Qy	972	GGATGACCTCGCAACTGACGTTATCTGACTGGGGCTGGCGGTGGAGATGAAGGGTGG	1031
Db	987	GGATGACCAACCGCCACATCCGATCTCTGACTGGACTAGTGTGCTGCTGCGCGAGG	1046
Qy	1032	CAAGCCCATCACAGAGGGCTGGAAACCAATGGTTTACATGCTCTGAGATCCTTAATGA	1091
Db	1047	CCAGACCATCAAGGGCGGTGGGCACCGTGGGTTTACATGGCTCGGAG---GTGGTGA	1103
Qy	1092	AAAGTAAAGTTATTCCTATCTGTGAGTGTGGTCCATGGATGGATCGAGATTTATGAAT	1151
Db	1104	GAATGAACGCTACAGTTTCAAGCTGAGTGGGCGCTCGGCTGCTCTGTACAGAT	1163
Qy	1152	GTTTGTGACGAAACCACTTCAAGATTTCAAGAAAGGTGACGTAAAGAGGATCTGAA	1211
Db	1164	GATCGAGCCAGTGGCCCTTCCAGCAGAGGAAGAGATCAAGCGGAGAGGTGA	1223
Qy	1212	GCAAGAACTCTGCAAGACGAGGTCAAAATCCAGCATGATAACTTTCACAGAGGAAGCAA	1271
Db	1224	GCGGCTGGTGAAGAGGTCCTCCGAGGAGTATTTCCGAGCGCTTTTCCCGCAGGCCGCTC	1283
Qy	1272	AGATATTTGAGGCTCTTCTTGGCTAAGAAACAGAGCAACGCTTAGGAGCAGAGAA	1331
Db	1284	ACTTTGTCTACAGCTCTCTCAAGAGGCCCTGCGCAACCGCTGGGGTGTGCTGGGGGCG	1343
Qy	1332	GTCTGATGATCCAGGAAACATCACTTTCTTAAACAGATCAACTTCTCGCTCGAAGC	1391
Db	1344	TGCCCGAGGTGAAGAGCACCCCTCTTTAAGAGCTGAATTTCAAGCGGCTGGAGC	1403
Qy	1392	TGGCCTAATTGAACCCCATTTGTGCCAGACCTTTCAGTGGTTTATGCAAGACATCGC	1451
Db	1404	TGGCATGTGAGCGCGCTTCAAGCCTGACCCCGAGGCCATTTACTGCAAGGATGTTCT	1463
Qy	1452	TGAATTTGATGATTTCTCTGAGTTTGGGGGTGAAATTTGATGACAAAGATAAGCAGTT	1511
Db	1464	GGACATTTGAACAGTTCTTACGCTCAAGGGGCTGGAGCTGAGCCCTACCGACGAGCTT	1523
Qy	1512	CTTCAAAACCTTGGCAGAGTGTGTTCTTATAGCATGGCAGGAAGAAATTTATAGAAC	1571
Db	1524	CTACAGAGTTTGCACAGGAGTGTGCCCATCCCTTGGCAGAACGAGATGGTGGAGAC	1583

QY 1572 GGACTGTTTGAGGAAGTGAATGAC 1596
Db 1584 CGAGTCTTCCAGAGCTGAATGTC 1608

RESULT 13

US-08-454-439-12
Sequence 12, Application US/08454439
Patent No. 5591618
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1758

US-08-454-439-12
Query Match 25.2%; Score 418.2; DB 1; Length 2204;
Best Local Similarity 56.2%; Pred. No. 2.9e-97;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

QY 15 GGCCCTGGCAACCTGATCGCCCAACACCGCCTACTCTGAGCGCCGAGAGCCCTCGGACTG 74
Db 33 GGAGCTCGAGACATCGTAGCGACACCGTGTACTCAAGCCCGGAGAGTGGCGTGG 92
QY 75 CGACAGCAAG---AGCTGCGAGCGCGCGGTAGCTGCGCCCTGCGCGGCTGCGAGG 131
Db 93 AATCGCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 152
QY 132 CTGGCGGAGCTCGCCAGAGAGCTGCTCCCTGAACTTCCAGAGCTGTGTAGGAGAGGCC 191

Db 153 GTGCGNAGAGCTGGGCTCAGCCTCGAGCGTGACTATCAGACCTGTGCGAGGCGCACCG 212
QY 192 CATCGGTGCGCGCTCTTTCGTGACTTCTTAGCCACAGTGCCTCAGTTCCTCCAGAGCGGC 251
Db 213 CATGGGCGCTGCTGTTCCGAGAGTCTGTGCGCACGAGGCGGAGCTGAGCGCTGCGT 272
QY 252 AACCTTCTAGAGAGCTGAGAGTGGAGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 311
Db 273 GCGCTTCTGATGGGCTGGCGGAGTGAAGTGAACCCCGGATGACAAAGCGNAGGCGATG 332
QY 312 CGCGCTGAGGCGCTGGTGGCCACTTGTGCGAGTGGCCCTGCGCCGCGGAGACCCGCAACC 371
Db 333 TGGGCGGACG---TAACGCGAGATTTCTGAGCCACACGGTCTGTGACTTATCCCTGA 389
QY 372 CTTCTGAGCAGCGCTGGCCACCAAGTGCACAGCAGCCACCACTGAGGAGAGAGCGAGT 431
Db 390 GGTCCCGCGGAGCTGGTGAACGAACTGCAACCCAGCGCTGGAGCAGGCTCCCTGCAAG 448
QY 432 GGCTGCAAGTACGCTGCGCAAGGCTGAGGCGCATGCTTCTTTCGCAAGCAGCAGCCCTTAA 491
Db 449 ACCTTTCCAGGAACCTACCGCGCTGA---CCAGAGTACTCTGAGCGTGGGCCCCCTTTGC 506
QY 492 GGATTTCTGACACGCGCTTTCTACGACAAAGTCTTCTGAGTGGAAACTCTTTCGAGATGCA 551
Db 507 CGACTACTCGACAGCATCTACTTCAACCGTTTCTGCGAGTGGAGTGGCTGGAAGGCA 566
QY 552 ACCAGTGTGACAGAGTACTTCTGAGTTCAGAGTCTGCGGAGAAAGGTGTTTTGGGA 611
Db 567 GCCAGTGACCAAAACACCTTTCAGGCAATACCGAGTCTCTGGTAAAGGTGGCTTTGGGA 626
QY 612 GGTATGTCGCTCCAGGTGAAACACTGCGGAGATGATGCTTGAAGAACTTGAACAA 671
Db 627 GGTGTGCGCTGCGAGTGGCGCCACAGTGAAGTATGCTTGAAGAACTTGAAGAA 686
QY 672 GAAGCGCTGAAGAAAGGTGGCGAGAGATGGCTCTCTTGAAGAAAGAAATCTTTGA 731
Db 687 AAGCGGATCAAGAAAGCGGAGGAGGCGCATGGCGCTGAAACGAGAGCAGATCTCTGA 746
QY 732 GAGGTGAGCAGCGCTTTTCATTTCTCTCTGGCTATGCTTTCGAGAGCAGAGCCCATCT 791
Db 747 GAAAGTGAACAGTAGGTTTGTAGTGTAGCTTGGGCTACGCTATGAGACCAAGGACGCGCT 806
QY 792 CTGCTTTGTGATGAGCTGATGAATGGGAGAGACCTCAAGTTCACATCTTACAACTGGG 851
Db 807 GTGCTGTGCTGACACTGATGAACGGGCGGAGCTCAAGTTCACATCTTACACATGGG 866
QY 852 CACGCTGGCTTGGACATGAGCGGCTGATCTTTTACTCGGCCAGATAGCCTGTGGAT 911
Db 867 CCGGCTGGCTTCCCGAAGCGGCGCGCTTCTTACGCGCGGAGATCTGTGCGCT 926
QY 912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGACATGAAGCTGAGAGTGTGCTTCT 971
Db 927 GAGGACCTGACCGGAGCGCATCGCATCTGACCTGGGACTAGCTGTGATGTCATGCGCGAG 986
QY 972 GGATGACCTCGCAACTGCAAGTATCTGACCTTGGGCTGGCGCTGGAGATGAAGGCTGG 1031
Db 987 GGATGACCAAGCGCACATCGCATCTGACCTGGGACTAGCTGTGATGTCATGCGCGAGG 1046
QY 1032 CAAGCCCATCAAGCAGGCTGGAACCAATGTTTATGAGTTCCTGAGATCTTATGGA 1091
Db 1047 CCAGACCATCAAGAGGCGGTGTGGGCGCCGCTTTCATGGCTTCCGAG---GTGGTGA 1103
QY 1092 AAAGGTAAAGTTATCTTCTATCTGTGACTGTTTTGCGGATGCGAGCTTATGAAAT 1151
Db 1104 GAATGAAGCTGACGTTGAGCCCTGACTGTGGGCGCTCGGCTGCTCTGTACGAGAT 1163
QY 1152 GGTGTGAGCAACCACTTCAAGATTAAGAGAAAGGTGAGTAAAGAGGATCTGAA 1211
Db 1164 GATCGGAGGCGCTGCGCTTCCAGCAGAGGAGAAAGAGATCAAGCGGAGGAGTGA 1223
QY 1212 GCAAGAACTCTGCAAGCAGAGTCAATTCAGCATGATTAACCTTACAGAGGAGCAAA 1271
Db 1224 CGGCTGGTGAAGAGGTCCCCGAGAGTATTCGAGCGCTTTTCCCGCAGGCGCGCTC 1283

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QY 1272 AGATATTGTCAGGCTCTTCTTGGCTAAGAAACACAGAGCAACGCTTAGGAAGCAGAGAAA 1331
D 1284 ACTTGTCTCACAGCTCTCTGCAAGGACCCCTGCGCAACGCTGGGGTGTCTGGGGGCGAG 1343
QY 1332 GTCTGATGATCCAGGAACATCATTTCTTAAACGATCAACTTCTCGCTGGAGC 1391
D 1344 TGCCCGCAGGTGAAGAGGACCCCTCTTTAAGAACTGAACCTTCAAGCGCTGGGAGC 1403
QY 1392 TGGCTTAATTGAACCCCAATTTGTGCCAGACCCCTTCACTGGTATTATGCCAAAGACATGCG 1451
D 1404 TGGCATGCTGGAGCGCGCTTCAAGCTTGACCCCGAGGCCATTACTGCAAGGATGTTCT 1463
QY 1452 TGAATTGATGATTTCTCTGAGTTTGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
D 1464 GGACATTTGAACAGATTTCTCTACGGTCAAGGGGTGGAGCTGGAGCCTACCGACGAGACTT 1523
QY 1512 CTTCAAAATTTGCGACAGGTGCTTCTTATAGCATGCGAGGAGAAATATAGAAC 1571
D 1524 CTACAGAAGTTTGCACAGGAGGTGCCCATCCCTGGCAGAACGAGATGGTGGAGAC 1583
QY 1572 GGGACTTTTGAAGAACTGAATGAC 1596
D 1584 CGAGTGTCTCAAGAGCTGAATGTC 1608

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RESULT 14

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PCT-US94-10487-12
; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10487
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,817
; FILING DATE: 31 MAR 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
PCT-US94-10487-12

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US-08-221-817-21
; Sequence 21, Application US/08221817
; Patent No. 5532151
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Werle F.
; TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,817
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 08/123,932
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532151and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 21:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
; LOCATION: 13..1740
; US-08-221-817-21

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	1659	100.0	2198	13 US-10-044-205A-1	Sequence 1, Appli
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4	1655.8	99.8	1662	17 US-10-451-168-49	Sequence 49, Appl
5	1655.8	99.8	1662	19 US-10-788-197-22	Sequence 22, Appl
6	1655.8	99.8	2249	9 US-09-802-117-5	Sequence 5, Appli
7	1655.8	99.8	2249	14 US-10-217-745-5	Sequence 5, Appli
8	1655.4	99.8	1662	9 US-09-802-117-1	Sequence 1, Appli
9	1655.4	99.8	1662	14 US-10-217-745-1	Sequence 1, Appli
10	1654.2	99.7	1662	9 US-09-964-469-1	Sequence 1, Appli
11	1654.2	99.7	1662	16 US-10-425-962-1	Sequence 1, Appli

12	1589.8	95.8	1701	17	US-10-072-012-273	Sequence 273, App
13	1046.8	63.1	1062	9	US-09-802-117-3	Sequence 3, Appli
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21	418.2	25.2	2848	10	US-09-873-367C-142	Sequence 142, App
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28	377.8	22.8	2519	13	US-10-071-766-13	Sequence 13, Appl
29	374.6	22.6	2519	10	US-03-971-392-72	Sequence 72, Appl
30	373	22.5	2511	14	US-10-072-036-60	Sequence 60, Appl
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33	373	22.5	2557	17	US-10-305-720-1298	Sequence 1298, Ap
34	373	22.5	2557	17	US-10-380-235-7	Sequence 7, Appli
35	373	22.5	2557	18	US-10-775-169-77	Sequence 77, Appl
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41	320.6	19.3	1737	19	US-10-788-197-18	Sequence 18, Appl
42	320.6	19.3	2017	19	US-10-677-983-8	Sequence 8, Appli
43	320.6	19.3	2113	16	US-10-325-430-1	Sequence 1, Appli
44	320.6	19.3	2113	19	US-10-677-983-7	Sequence 7, Appli
45	311.6	18.8	1503	19	US-10-788-197-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

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; Sequence 3, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPPELLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; FILE REFERENCE: 10147-5201
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,894
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
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US-10-044-205A-3

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 541 TTCGAGTGCACACAGTTCAGACAGTACTTCACTGAGTTCAGAGTTCGAGGAAAGT 600
Db 541 TTCGAGTGCACACAGTTCAGACAGTACTTCACTGAGTTCAGAGTTCGAGGAAAGT 600
QY 601 GGTTTTGGGAGGTATGTGCCCTCCAGGTGAAACACTGGGAAGATGTATGCTGTAAG 660
Db 601 GGTTTTGGGAGGTATGTGCCCTCCAGGTGAAACACTGGGAAGATGTATGCTGTAAG 660
QY 661 AAATGGAACAAGCGGTGAAGAGAAAGTGGCGAGAGATGGCTCTCTTGAAGAG 720
Db 661 AAATGGAACAAGCGGTGAAGAGAAAGTGGCGAGAGATGGCTCTCTTGAAGAG 720
QY 721 GAATCTTGGAGAGTCAAGCGCTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 GAATCTTGGAGAGTCAAGCGCTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 AAGACCCATCTCTGCTTCTATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC 840
Db 781 AAGACCCATCTCTGCTTCTATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC 840
QY 841 TACAAGTGGGACGGGTGGCTGACATGACCGGGTATCTTTTACTCGGCCAGATA 900
Db 841 TACAAGTGGGACGGGTGGCTGACATGACCGGGTATCTTTTACTCGGCCAGATA 900
QY 901 GCTGTGGATGCTGACCTCCATGACTCGCATCTCTATCGGACATGAAGCTGAG 960
Db 901 GCTGTGGATGCTGACCTCCATGACTCGCATCTCTATCGGACATGAAGCTGAG 960
QY 961 AATGTCTTCTGATGACCTCGGCAACTGACGTTATCTGACCTGGGGTGGCGGTGAG 1020
Db 961 AATGTCTTCTGATGACCTCGGCAACTGACGTTATCTGACCTGGGGTGGCGGTGAG 1020
QY 1021 ATGAAGGTGGCAGCCCATCCAGAGGCTGGAACCAATGGTTTACATGGCTCTGAG 1080
Db 1021 ATGAAGGTGGCAGCCCATCCAGAGGCTGGAACCAATGGTTTACATGGCTCTGAG 1080
QY 1081 ATCTTAATGAAGAGTAAAGTATTCTTCTGCTGAGTGGTTTCCATGGATGCAGC 1140
Db 1081 ATCTTAATGAAGAGTAAAGTATTCTTCTGCTGAGTGGTTTCCATGGATGCAGC 1140
QY 1141 ATTTATGAATGGTGTGCTGGACGAAACCACTTCAAGAAAGGTGAGTAA 1200

Db 1141 ATTTATGAATGGTGTGCTGGACGAAACCACTTCAAGAAAGGTGAGTAA 1200
QY 1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTCAAAATTCAGCATGATACTTACA 1260
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTCAAAATTCAGCATGATACTTACA 1260
QY 1261 GAGGAACAAAGATATTTGACGGCTCTTCTTGGCTAAGAAACAGAGCAACGTTAGGA 1320
Db 1261 GAGGAACAAAGATATTTGACGGCTCTTCTTGGCTAAGAAACAGAGCAACGTTAGGA 1320
QY 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCACTTTCCT 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCACTTTCCT 1380
QY 1381 CGCTGGAAGTGGCTTAATTTGAACCCCACTTTGTGCGAGACCTTCACTGGTTATGCC 1440
Db 1381 CGCTGGAAGTGGCTTAATTTGAACCCCACTTTGTGCGAGACCTTCACTGGTTATGCC 1440
QY 1441 AAAGACATCGTGAATTTGATGATTTCTGAGGTTCTGGGGGTGGAAATTTGATGACAAA 1500
Db 1441 AAAGACATCGTGAATTTGATGATTTCTGAGGTTCTGGGGGTGGAAATTTGATGACAAA 1500
QY 1501 GATGAAGCATTTCTTCAAAACTTTGCGACAGGTGCTGTTCTATAGCATGCGAGAGAA 1560
Db 1501 GATGAAGCATTTCTTCAAAACTTTGCGACAGGTGCTGTTCTATAGCATGCGAGAGAA 1560
QY 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGTGAG 1620
Db 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGTGAG 1620
QY 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659
Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 2
US-10-044-205A-1
; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMAN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-1

Query Match 100.0%; Score 1659; DB 13; Length 2198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGATGCGGGGCTTGGACAACTGATCGCCACACCGCTACTCTGAGGCCGG 60
Db 291 ATGTGGATGCGGGGCTTGGACAACTGATCGCCACACCGCTACTCTGAGGCCGG 350
QY 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAAGCGCGCGGTAGCCTTGGCCCTGCC 120
Db 351 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAAGCGCGCGGTAGCCTTGGCCCTGCC 410

QY 121 GGGCTGCAGGGCTGCGCGAGCTCGCCGAGAGCTCGCCGAGAGCTGCTCCCTGAACTTTCCACAGCCTGTGT 180
DB 411 GGGCTGCAGGGCTGCGCGAGCTCGCCGAGAGCTCGCCGAGAGCTGCTCCCTGAACTTTCCACAGCCTGTGT 470
QY 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCTGCTGACTTCTAGCCAGCAGTGCACAGTGC 240
DB 471 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCTGCTGACTTCTAGCCAGCAGTGCACAGTGC 530
QY 241 CCGAAGGGGCGCAACCTTCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCC 300
DB 531 CCGAAGGGGCGCAACCTTCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCC 590
QY 301 ACCAAAGACAGCGCTGAGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGG 360
DB 591 ACCAAAGACAGCGCTGAGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGG 650
QY 361 AACCCGCAACCTTCTAGCCAGCAGCGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGG 420
DB 651 AACCCGCAACCTTCTAGCCAGCAGCGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGG 710
QY 421 GAAGAGCAGTGGCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 480
DB 711 GAAGAGCAGTGGCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 770
QY 481 CAGCCCTTTAAGATTTGCTGACAGCGCTTCTACGACAGTTCCTGAGTGCAGTGCAGTGCAGTGC 540
DB 771 CAGCCCTTTAAGATTTGCTGACAGCGCTTCTACGACAGTTCCTGAGTGCAGTGCAGTGCAGTGC 830
QY 541 TTCGAGTGCACACAGTGCAGACAGTTCCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 600
DB 831 TTCGAGTGCACACAGTGCAGACAGTTCCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 890
QY 601 GGTTTTGGGAGGTATGTGCTGCTGATGAGCTGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 660
DB 891 GGTTTTGGGAGGTATGTGCTGCTGATGAGCTGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 950
QY 661 AAATGGACAGAGCGCTGAG 720
DB 951 AAATGGACAGAGCGCTGAG 1010
QY 721 GAAATCTTGGAGAGGTGAG 780
DB 1011 GAAATCTTGGAGAGGTGAG 1070
QY 781 AAGACCCATCTGCTGCTGATGAGCTGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 840
DB 1071 AAGACCCATCTGCTGCTGATGAGCTGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1130
QY 841 TACAAAGTGGGACGCTGCTGAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 900
DB 1131 TACAAAGTGGGACGCTGCTGAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1190
QY 901 GCCTGTGGAGTGCAGCCTGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 960
DB 1191 GCCTGTGGAGTGCAGCCTGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1250
QY 961 AATGTGCTTCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1020
DB 1251 AATGTGCTTCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1310
QY 1021 ATGAAGGGTGGCAAGCCATCACCAGAGGGCTGGAACCAATGGTTTACATGGCTCCTGAG 1080
DB 1311 ATGAAGGGTGGCAAGCCATCACCAGAGGGCTGGAACCAATGGTTTACATGGCTCCTGAG 1370
QY 1081 ATCTTAATGGAAGAGTAAAGTTATTCCTATCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1140
DB 1371 ATCTTAATGGAAGAGTAAAGTTATTCCTATCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1430
QY 1141 ATTTATGAATGGTGTGCTGAGCAGACACCATTCAGAGTTACAGGAAAGGTTCAGTAA 1200
DB 1431 ATTTATGAATGGTGTGCTGAGCAGACACCATTCAGAGTTACAGGAAAGGTTCAGTAA 1490

QY 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCAGGCTCAAAATTCAGCATGATTAACCTTCA 1260
DB 1491 GAGGATCTGAAGCAAGAACTCTGCAAGCAGGCTCAAAATTCAGCATGATTAACCTTCA 1550
QY 1261 GAGGAAGCAAGAAATATTTGAGGCTCTTTGAGGCTTAAGAAACCAAGCAAGCTTTAGGA 1320
DB 1551 GAGGAAGCAAGAAATATTTGAGGCTCTTTGAGGCTTAAGAAACCAAGCAAGCTTTAGGA 1610
QY 1321 AGCAGAGAAAAGTCTGATGATCCCGAGGAAACATCAATTTCTTTAAACGATCAACTTTCT 1380
DB 1611 AGCAGAGAAAAGTCTGATGATCCCGAGGAAACATCAATTTCTTTAAACGATCAACTTTCT 1670
QY 1381 CCGCTGGAAGCTGGCTAATTTGAACCCCAATTTGTCAGACCCCTTCAGTGTATGTC 1440
DB 1671 CCGCTGGAAGCTGGCTAATTTGAACCCCAATTTGTCAGACCCCTTCAGTGTATGTC 1730
QY 1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGCTGGAATTTGATGACAAA 1500
DB 1731 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGCTGGAATTTGATGACAAA 1790
QY 1501 GATAAGCAGTTCTTCAAAAACCTTTTCGACAGGCTGCTGTTCTATAGCATGGCAGGAAGAA 1560
DB 1791 GATAAGCAGTTCTTCAAAAACCTTTTCGACAGGCTGCTGTTCTATAGCATGGCAGGAAGAA 1850
QY 1561 ATTATAGAAAACGAGTCTGTTGAGGAACTGAATGATGACCCCAAGACCTTACGGGTTGTGAG 1620
DB 1851 ATTATAGAAAACGAGTCTGTTGAGGAACTGAATGATGACCCCAAGACCTTACGGGTTGTGAG 1910
QY 1621 GAGGTAATTCATCAAGTCTGGGCTGTTGTTTATTG 1659
DB 1911 GAGGTAATTCATCAAGTCTGGGCTGTTGTTTATTG 1949

RESULT 3

US-10-311-034-45

; Sequence 45, Application US/10311034

; Publication No. US20040023242A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: YUE, Henry

; APPLICANT: LAL, Preeti

; APPLICANT: BANDMAN, Olga

; APPLICANT: BOROWSKI, Mark L.

; APPLICANT: AU-YOUNG, Janice

; APPLICANT: LU, Yan

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: YAO, Monique G.

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: GREENWALD, Sara R.

; APPLICANT: RAMKUMAR, Javalaxmi

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: KEARNEY, Liam

; APPLICANT: BURFORD, Neil

; APPLICANT: NGUYEN, Darniel B.

; APPLICANT: TANG, Y. Tom

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: HE, Ann

; APPLICANT: THORNTON, Michael

; APPLICANT: HAPALIA, April

; APPLICANT: ARVIZU, Chandra S.

; APPLICANT: GURURAJAN, Rajagopal

; APPLICANT: LO, Terence P.

; APPLICANT: KHAH, Farrah A.

; APPLICANT: RECIPON, Shirley A.

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: POLICKY, Jennifer L.

; APPLICANT: DING, Li

; APPLICANT: GREYER, Megan

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: THANGAVELU, Kavitha

; APPLICANT: BATRA, SaJeew

APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

Query Match 99.8%; Score 1655.8; DB 17; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGTGGACATGGGGCCCTGGACAACTGATCGCAACACGCGCTACTGCGAGCCCGG 60
DB 1 ATGGTGGACATGGGGCCCTGGACAACTGATCGCAACACGCGCTACTGCGAGCCCGG 60
QY 61 AAGCCTCGGACTGCGACGAGCAAGAGCTGCGAGCGCGCGGTAGCCTGCGCC 120
DB 61 AAGCCTCGGACTGCGACGAGCAAGAGCTGCGAGCGCGCGGTAGCCTGCGCC 120
QY 121 GGGTGCAGGGCTGCGCGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCTGT 180
DB 121 GGGTGCAGGGCTGCGCGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCTGT 180
QY 181 GAGCAGAGCCCATCGGTGCGCGCTCTTCCTGAGCTTCTAGCCACAGTGCCACGTT 240
DB 181 GAGCAGAGCCCATCGGTGCGCGCTCTTCCTGAGCTTCTAGCCACAGTGCCACGTT 240
QY 241 CGAAGCGGCAACCTTCTAGAGAGCTGCGAGAACTGGAGCTGGCGAGGAGGCC 300
DB 241 CGAAGCGGCAACCTTCTAGAGAGCTGCGAGAACTGGAGCTGGCGAGGAGGCC 300
QY 301 ACCAAGACAGCGCTGCGAGGGCTGCGCCACTTGTGCGAGTGCCCTGCCCGGG 360
DB 301 ACCAAGACAGCGCTGCGAGGGCTGCGCCACTTGTGCGAGTGCCCTGCCCGGG 360
QY 361 AACCCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTCCAGCAGCCACCACTGAG 420
DB 361 AACCCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTCCAGCAGCCACCACTGAG 420
QY 421 GAAGAGCGAGTGCGTGCAGTGCCTGCGCAAGCTGAGGCGCATGGCTTTCTTGAAG 480
DB 421 GAAGAGCGAGTGCGTGCAGTGCCTGCGCAAGCTGAGGCGCATGGCTTTCTTGAAG 480
QY 481 CAGCCCTTAAAGATTTCGTGACAGCGCTTCTACGCAAGTTTCTGCACTGGAATC 540
DB 481 CAGCCCTTAAAGATTTCGTGACAGCGCTTCTACGCAAGTTTCTGCACTGGAATC 540
QY 541 TTCGAGATGCAACCACTGTCAGCAAGTACTTCACTGAGTTTCAGAGTGTGCGGAAAGGT 600
DB 541 TTCGAGATGCAACCACTGTCAGCAAGTACTTCACTGAGTTTCAGAGTGTGCGGAAAGGT 600
QY 601 GGTGGGAGGATATGTCGCTCAGGTGCAAGAACTGCGGAAAGATGTATGCTGTAAAG 660
DB 601 GGTGGGAGGATATGTCGCTCAGGTGCAAGAACTGCGGAAAGATGTATGCTGTAAAG 660
QY 661 AAATCGGCAAGAGCGCTGAAGAGAAAGTGGCGAGAGTGGCTCTCTTGGAAAG 720
DB 661 AAATCGGCAAGAGCGCTGAAGAGAAAGTGGCGAGAGTGGCTCTCTTGGAAAG 720
QY 721 GAAATCTTGGAGAGGTGAGCGCCCTTTCATTGTCTCTGCGCCTATGCTTTGAGAGC 780

DB 721 GAAATCTTGGAGAGGTGAGCGCCCTTTCATTGTCTCTGCGCTATGCTTTGAGAGC 780
QY 781 AAGACCCATCTCTGCTTGTCTATGAGCTGATGATGAGGAGAGCTCAAGTTTCCATC 840
DB 781 AAGACCCATCTCTGCTTGTCTATGAGCTGATGATGAGGAGAGCTCAAGTTTCCATC 840
QY 841 TACACGTGGGCGCGCTGCGCATGAGCATGAGCGGGTGATCTTTACTCGGCCAGATA 900
DB 841 TACACGTGGGCGCGCTGCGCATGAGCATGAGCGGGTGATCTTTACTCGGCCAGATA 900
QY 901 GCCTGTGGATGCTGCACTCCATCACTCGGCATCGTCTATCGGGAATGAAGCCTGAG 960
DB 901 GCCTGTGGATGCTGCACTCCATCACTCGGCATCGTCTATCGGGAATGAAGCCTGAG 960
QY 961 AATGTCTTCTGGATGAGCTCGGCACTGCAAGTTATCTGACCTGGGCTGGCGTGAG 1020
DB 961 AATGTCTTCTGGATGAGCTCGGCACTGCAAGTTATCTGACCTGGGCTGGCGTGAG 1020
QY 1021 ATGAGGGTGGCAAGCCCATCAGCAGAGGCTGGAACCAATGGTTACATGGCTCTGAG 1080
DB 1021 ATGAGGGTGGCAAGCCCATCAGCAGAGGCTGGAACCAATGGTTACATGGCTCTGAG 1080
QY 1081 ATCTTAATGGAAGAGTAAGTTTATCTCTATCTCTGAGCTGGTTGCCATGGGATGAGC 1140
DB 1081 ATCTTAATGGAAGAGTAAGTTTATCTCTATCTCTGAGCTGGTTGCCATGGGATGAGC 1140
QY 1141 ATTTATGAATGGTGTGCGAGCAACCACTTCAAGATTAAGAGAAAGGTCAGTAAA 1200
DB 1141 ATTTATGAATGGTGTGCGAGCAACCACTTCAAGATTAAGAGAAAGGTCAGTAAA 1200
QY 1201 GAGCATCTGAGCAAGAACTCTCAAGAGCAGGTCAAATTCAGCATGATTAACCTTACA 1260
DB 1201 GAGCATCTGAGCAAGAACTCTCAAGAGCAGGTCAAATTCAGCATGATTAACCTTACA 1260
QY 1261 GAGGAAGCAAGAGATATTTGAGGCTCTTCTGAGCTTGAAGAACCAAGCAAGCTTAGGA 1320
DB 1261 GAGGAAGCAAGAGATATTTGAGGCTCTTCTGAGCTTGAAGAACCAAGCAAGCTTAGGA 1320
QY 1321 AGCAGAGAAAGTCTGATGATCCAGAGAACTATTTCTTTAAACGATCAACTTTCCT 1380
DB 1321 AGCAGAGAAAGTCTGATGATCCAGAGAACTATTTCTTTAAACGATCAACTTTCCT 1380
QY 1381 CGCTGGAAGCTGCGCTAAATTTGAACCCCTCTTGTGCGAGAGCTTCACTGCTTATGCC 1440
DB 1381 CGCTGGAAGCTGCGCTAAATTTGAACCCCTCTTGTGCGAGAGCTTCACTGCTTATGCC 1440
QY 1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500
DB 1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500
QY 1501 GATAAGCAGTTCTTCAAAAACCTTTGCGAGAGTGTCTCTATAGCATGCGAGAGAA 1560
DB 1501 GATAAGCAGTTCTTCAAAAACCTTTGCGAGAGTGTCTCTATAGCATGCGAGAGAA 1560
QY 1561 ATTATAGAAAGCGAGCTGTTTGAAGAACTGAATCAACCCCAAGCTTACGCTGCTGAG 1620
DB 1561 ATTATAGAAAGCGAGCTGTTTGAAGAACTGAATCAACCCCAAGCTTACGCTGCTGAG 1620
QY 1621 GAGGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659
DB 1621 GAGGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 4
US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS

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; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-49

Query Match      99.8%; Score 1655.8; DB 17; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  ATGTGGACATGGGGCCCTGCACAACTGATCGCAACACCGCCTACTCGAGGCCGG 60
Db      1  ATGTGGACATGGGGCCCTGCACAACTGATCGCAACACCGCCTACTCGAGGCCGG 60

Qy      61  AAGCCCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGGCTAGCCTGCGCC 120
Db      61  AAGCCCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGGCTAGCCTGCGCC 120

Qy     121  GGGCTGACGGGTGCGCGAGCTCGCCGAGAGCTGCTGAACTTCACAGCCCTGTGT 180
Db     121  GGGCTGACGGGTGCGCGAGCTCGCCGAGAGCTGCTGAACTTCACAGCCCTGTGT 180

Qy     181  GAGCAGCAGCCCATCGTTCGCGCCTCTTCGCTGACTTCCTAGCCACAGTGCACGTTT 240
Db     181  GAGCAGCAGCCCATCGTTCGCGCCTCTTCGCTGACTTCCTAGCCACAGTGCACGTTT 240

Qy     241  CGCAAGGCGGCAACCTTCTTAGAGGACGTGCGAGAACTGGGAGCTGGCGAGGAGGCC 300
Db     241  CGCAAGGCGGCAACCTTCTTAGAGGACGTGCGAGAACTGGGAGCTGGCGAGGAGGCC 300

Qy     301  ACCAAGACAGCGCGCTGAGGGGCTGTGGCCACTGTGTGAGTGCCTGCGCCCGGG 360
Db     301  ACCAAGACAGCGCGCTGAGGGGCTGTGGCCACTGTGTGAGTGCCTGCGCCCGGG 360

Qy     361  AACCCGCAACCTTCTTCCAGCAGCGCTGGCCACCAAGTGCCAGCAGCCACCACTGAG 420
Db     361  AACCCGCAACCTTCTTCCAGCAGCGCTGGCCACCAAGTGCCAGCAGCCACCACTGAG 420

Qy     421  GAAGAGCGAGTGGCTGCAGTACGCTGGCGCAAGGCTGAGGCCCATGGCTTTCTTGAAGAG 480
Db     421  GAAGAGCGAGTGGCTGCAGTACGCTGGCGCAAGGCTGAGGCCCATGGCTTTCTTGAAGAG 480

Qy     481  CAGCCCTTAAGGATTTCTGACAGCGCTTCTACGACAAAGTTTCTGCAAGTGGAACTC 540
Db     481  CAGCCCTTAAGGATTTCTGACAGCGCTTCTACGACAAAGTTTCTGCAAGTGGAACTC 540

Qy     541  TTCGAGATGCACACAGTGTACAGCAAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGT 600
Db     541  TTCGAGATGCACACAGTGTACAGCAAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGT 600
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Qy      601  GGTTTGGGAGGTATGTGCGCTCAGGTGAAAAACACTGGGAAGATGTATGCTGTAAAG 660
Db      601  GGTTTGGGAGGTATGTGCGCTCAGGTGAAAAACACTGGGAAGATGTATGCTGTAAAG 660

Qy      661  AAACCTGGACAAGAGCGCTGAAGAAGAAAGTGGCGAAGAGATGGCTCTCTTTGAAAAG 720
Db      661  AAACCTGGACAAGAGCGCTGAAGAAGAAAGTGGCGAAGAGATGGCTCTCTTTGAAAAG 720

Qy      721  GAAATCTTTGGAGAAGGTGAGAGAGCCCTTTCTATTTGTCTCTCTGGCCCTATGCTT 780
Db      721  GAAATCTTTGGAGAAGGTGAGAGAGCCCTTTCTATTTGTCTCTCTGGCCCTATGCTT 780

Qy      781  AAGACCCATCTCTGCTTGTATGAGCCCTGATGAATGGGGAGAGACTCAAGTTCCACATC 840
Db      781  AAGACCCATCTCTGCTTGTATGAGCCCTGATGAATGGGGAGAGACTCAAGTTCCACATC 840

Qy      841  TACAAGTGGGACGCGCTGGACATGAGCGGGGTGATCTTTTACTTCGGCCCCAGATA 900
Db      841  TACAAGTGGGACGCGCTGGACATGAGCGGGGTGATCTTTTACTTCGGCCCCAGATA 900

Qy      901  GCCTGTGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG 960
Db      901  GCCTGTGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG 960

Qy      961  AATGTCTTCTGGATGACCTCGGCAACTGCGAGGTTATCTGACCTGGGGCTGGCCGTGAG 1020
Db      961  AATGTCTTCTGGATGACCTCGGCAACTGCGAGGTTATCTGACCTGGGGCTGGCCGTGAG 1020

Qy     1021  ATGAAGGGTGCAGAGCCCATCACCCAGAGGCTGGAACCAATGTTTACATGGCTCTGAG 1080
Db     1021  ATGAAGGGTGCAGAGCCCATCACCCAGAGGCTGGAACCAATGTTTACATGGCTCTGAG 1080

Qy     1081  ATCTTAATGAAAAAGTAAAGTTATTTCTTATCTCTGTGACTGGTTGCCATGGGATGAGC 1140
Db     1081  ATCTTAATGAAAAAGTAAAGTTATTTCTTATCTCTGTGACTGGTTGCCATGGGATGAGC 1140

Qy     1141  ATTTATGAATGTTTGTGCGAAGCAACCATTTCAAAGATTACAAGAAAAAGGTGAGTAA 1200
Db     1141  ATTTATGAATGTTTGTGCGAAGCAACCATTTCAAAGATTACAAGAAAAAGGTGAGTAA 1200

Qy     1201  GAGGATCTGAAGCAAGAACTCTCAAGCAGAGGTCAAAATTCACAGCATGATACTTACA 1260
Db     1201  GAGGATCTGAAGCAAGAACTCTCAAGCAGAGGTCAAAATTCACAGCATGATACTTACA 1260

Qy     1261  GAGGAAGCAAAAGATATTTGAGGCTCTTTGCGCTTAAAGAAACCAAGAGCAACGCTTAG 1320
Db     1261  GAGGAAGCAAAAGATATTTGAGGCTCTTTGCGCTTAAAGAAACCAAGAGCAACGCTTAG 1320

Qy     1321  AGCAGAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCGATCAACTTCTCT 1380
Db     1321  AGCAGAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCGATCAACTTCTCT 1380

Qy     1381  CGCTGGAGCTGGCTTAATTTGAACCCCATTTGCGCAGAGCCCTTCAAGTGGTTATGCC 1440
Db     1381  CGCTGGAGCTGGCTTAATTTGAACCCCATTTGCGCAGAGCCCTTCAAGTGGTTATGCC 1440

Qy     1441  AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500
Db     1441  AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500

Qy     1501  GATAGAGAGTTCTTCAAAAACTTTTGCAGAGCTGCTGTTCTTATAGCATGGCAGAGAA 1560
Db     1501  GATAGAGAGTTCTTCAAAAACTTTTGCAGAGCTGCTGTTCTTATAGCATGGCAGAGAA 1560

Qy     1561  ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGTTGTGAG 1620
Db     1561  ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGTTGTGAG 1620

Qy     1621  GAGGTAATTCATCCAAAGTCTGGGCTGTGTTGTTTATTG 1659
Db     1621  GAGGTAATTCATCCAAAGTCTGGGCTGTGTTGTTTATTG 1659
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RESULT 5

US-10-788-197-22
; Sequence 22, Application US/10788197
; Publication No. US20050032125A1
; GENERAL INFORMATION:
; APPLICANT: OAKLEY, ROBERT H.
; APPLICANT: HUDSON, CHRISTINE C.
; TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
; FILE REFERENCE: NRK 108
; CURRENT APPLICATION NUMBER: US/10/788,197
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/14581
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,986
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/401,698
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-197-22

Query Match 99.8%; Score 1655.8; DB 19; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGTGGACATCGGGGCCCTGGACAACTGTATCGCAACACCGCTTACCTGACGCGCCGG	60
DB	1	ATGTGGACATCGGGGCCCTGGACAACTGTATCGCAACACCGCTTACCTGACGCGCCGG	60
QY	61	AGCCCTCGGACTGGACAGCAAGAGCTGCGCGCGCGCGCGGTAGCCCTGCCCC	120
DB	61	AGCCCTCGGACTGGACAGCAAGAGCTGCGCGCGCGCGGTAGCCCTGCCCC	120
QY	121	GGCTGCGAGGCTGGCGGAGCTCGCGCAAGAGCTGCTCCGAACTTCCACAGCCTGT	180
DB	121	GGCTGCGAGGCTGGCGGAGCTCGCGCAAGAGCTGCTCCGAACTTCCACAGCCTGT	180
QY	181	GAGCAGCAGCCCATCGGTGCGGCTCTTCCGTGACTTCTAGCAGCAGTGCACAGTTC	240
DB	181	GAGCAGCAGCCCATCGGTGCGGCTCTTCCGTGACTTCTAGCAGCAGTGCACAGTTC	240
QY	241	CGCAGGCGGCAACCTTCTAGAGACGTGCGAGAACTGGGAGCTGGCGAGGGAGCCC	300
DB	241	CGCAGGCGGCAACCTTCTAGAGACGTGCGAGAACTGGGAGCTGGCGAGGGAGCCC	300
QY	301	ACCAAGACAGCGCGCTGCGAGGCGTGGTGGCCACTTGTGCGAGTGCCTGCCCGGG	360
DB	301	ACCAAGACAGCGCGCTGCGAGGCGTGGTGGCCACTTGTGCGAGTGCCTGCCCGGG	360
QY	361	AACCGCAACCTTCTCAGCAGCGCGTGGCCCAAGAGTGCAGAGCAGCAGTGCAG	420
DB	361	AACCGCAACCTTCTCAGCAGCGCGTGGCCCAAGAGTGCAGAGCAGCAGTGCAG	420
QY	421	GAGAGCGAGTGGCTGCGAGTGCAGTGCAGGCTGCGAGGCTGAGGCCATGGCTTCTT	480
DB	421	GAGAGCGAGTGGCTGCGAGTGCAGTGCAGGCTGCGAGGCTGAGGCCATGGCTTCTT	480
QY	481	CAGCCCTTTAAGGATTTCTGACAGCGCTTCTACGACCAAGTTCCTCAGTGGAACTC	540
DB	481	CAGCCCTTTAAGGATTTCTGACAGCGCTTCTACGACCAAGTTCCTCAGTGGAACTC	540
QY	541	TTGAGATGCAACAGTGTGAGCAAGTATCTTCACTGAGTTCAGAGTCTGGGAAAGGT	600
DB	541	TTGAGATGCAACAGTGTGAGCAAGTATCTTCACTGAGTTCAGAGTCTGGGAAAGGT	600
QY	601	GGTTTTGGGAGGTATGTGCGCTCCAGGTGAGAACTGGGAGATGATGCTGCTTAAG	660
DB	601	GGTTTTGGGAGGTATGTGCGCTCCAGGTGAGAACTGGGAGATGATGCTGCTTAAAG	660

RESULT 6

US-09-802-117-5
; Sequence 5, Application US/09802117
; Publication No. US20020042503A1

QY	661	AACTGGAGCAAGAGCGGCTGAAGAGAAAGGTGGCGAGAGATGGCTCTCTTTGAAAAG	720
DB	661	AACTGGAGCAAGAGCGGCTGAAGAGAAAGGTGGCGAGAGATGGCTCTCTTTGAAAAG	720
QY	721	GAATCTTTGGAGAGGTTCAGCAGCCCTTTCACTCTCTCTGCGCTATGCTTTGAGAGC	780
DB	721	GAATCTTTGGAGAGGTTCAGCAGCCCTTTCACTCTCTCTGCGCTATGCTTTGAGAGC	780
QY	781	AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGAGAGACCTCAAGTTCACATC	840
DB	781	AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGAGAGACCTCAAGTTCACATC	840
QY	841	TACAAGTGGGCGCGCTGGACATGAGCGGGTGTATCTTTACTTCGCGCCAGATA	900
DB	841	TACAAGTGGGCGCGCTGGACATGAGCGGGTGTATCTTTACTTCGCGCCAGATA	900
QY	901	GCCTGTGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG	960
DB	901	GCCTGTGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG	960
QY	961	AATGTGCTTCTGGATGACCTCGGCAACTGCGAGGTATCTGACCTGGGCTGGCGTGGAG	1020
DB	961	AATGTGCTTCTGGATGACCTCGGCAACTGCGAGGTATCTGACCTGGGCTGGCGTGGAG	1020
QY	1021	ATGAAGGTGGCAAGCCCATCACCCAGAGGCTCGAAACCAATGTTACATGCTCTCTGAG	1080
DB	1021	ATGAAGGTGGCAAGCCCATCACCCAGAGGCTCGAAACCAATGTTACATGCTCTCTGAG	1080
QY	1081	ATCCTAATGGAAGGTAAAGTTATTCCTATCTCTGAGCTGTTTGGCATGGGATGAGC	1140
DB	1081	ATCCTAATGGAAGGTAAAGTTATTCCTATCTCTGAGCTGTTTGGCATGGGATGAGC	1140
QY	1141	ATTTATGAAATGGTGTGGACGACCACTTCAAGATTTACAAGAAAGGTCACTAAA	1200
DB	1141	ATTTATGAAATGGTGTGGACGACCACTTCAAGATTTACAAGAAAGGTCACTAAA	1200
QY	1201	GAGGATCTGAAGCAAGAACTCTCAAGACAGAGTCAAAATCCAGCATGATACTTACA	1260
DB	1201	GAGGATCTGAAGCAAGAACTCTCAAGACAGAGTCAAAATCCAGCATGATACTTACA	1260
QY	1261	GAGGACCAAGAAATTTGCGAGCTCTTCTGCTTAAGAAACAGAGCAACGTTTAGGA	1320
DB	1261	GAGGACCAAGAAATTTGCGAGCTCTTCTGCTTAAGAAACAGAGCAACGTTTAGGA	1320
QY	1321	AGCAGAGAAAGTCTGATGATCCAGAGAAACATCTTTCTTAAACGATCAACTTCTCT	1380
DB	1321	AGCAGAGAAAGTCTGATGATCCAGAGAAACATCTTTCTTAAACGATCAACTTCTCT	1380
QY	1381	CGCCTGGAAGCTGGCCTAAATTTGAACCCCAATTTGTGCGAGACCCCTTCAGTGGTTATGCC	1440
DB	1381	CGCCTGGAAGCTGGCCTAAATTTGAACCCCAATTTGTGCGAGACCCCTTCAGTGGTTATGCC	1440
QY	1441	AAAGACATCGTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA	1500
DB	1441	AAAGACATCGTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAAATTTGATGACAAA	1500
QY	1501	GATAAGCAGTCTTCAAAACTTTCCACAGAGTCTCTCTTATAGCATGCGAGGAGAA	1560
DB	1501	GATAAGCAGTCTTCAAAACTTTCCACAGAGTCTCTCTTATAGCATGCGAGGAGAA	1560
QY	1561	ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTGTGAG	1620
DB	1561	ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTGTGAG	1620
QY	1621	GAGGTAATTCATCCAAAGTCTGGCGTGTGTTTATTG	1659
DB	1621	GAGGTAATTCATCCAAAGTCTGGCGTGTGTTTATTG	1659

GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Query Match 99.8%; Score 1655.8; DB 9; Length 2249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGTTGGACATGGGGGCTGGACAACTGATCGCCCAACACCGCTACTGCGAGCCCGG 60
Db 354 ATGTTGGACATGGGGGCTGGACAACTGATCGCCCAACACCGCTACTGCGAGCCCGG 413
Qy 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGCGTAGCTGSCCTGCGCC 120
Db 414 AAGCCCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGCGTAGCTGSCCTGCGCC 473
Qy 121 GGGCTGACAGGGTGGCGGAGCTCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
Db 474 GGGCTGACAGGGTGGCGGAGCTCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 533
Qy 191 GAGCAGAGCCCATCGTTCGCGCTCTTCCTGAGCTTCCTGAGCAGAGTGCCTGAGTTC 240
Db 534 GAGCAGAGCCCATCGTTCGCGCTCTTCCTGAGCTTCCTGAGCAGAGTGCCTGAGTTC 593
Qy 241 CGAAGCGCGCAACCTTCTAGAGCAGTGCAGAACTGGAGCTGGCGAGGAGGACCC 300
Db 594 CGAAGCGCGCAACCTTCTAGAGCAGTGCAGAACTGGAGCTGGCGAGGAGGACCC 653
Qy 301 ACCAAGACAGCGCTGACAGGGCTGTGGCCACTTGTGGAGTGCCTGCCCCGGGG 360
Db 654 ACCAAGACAGCGCTGACAGGGCTGTGGCCACTTGTGGAGTGCCTGCCCCGGGG 713
Qy 361 AACCGCAACCTTCTCAGCAGCGCTGGCCACCAAGTGCAGAGCAGCCACCACTGAG 420
Db 714 AACCGCAACCTTCTCAGCAGCGCTGGCCACCAAGTGCAGAGCAGCCACCACTGAG 773
Qy 421 GAAGAGCAGTGGCTGACGAGTGCAGCTGCGCAAGGCTGAGGCGCATGCTTCTTGAAG 480
Db 774 GAAGAGCAGTGGCTGACGAGTGCAGCTGCGCAAGGCTGAGGCGCATGCTTCTTGAAG 833
Qy 481 CAGCCCTTTAAGGATTTCTGACCAAGCTTCTACGACAACTTCTGAGTGCAGAACTC 540
Db 834 CAGCCCTTTAAGGATTTCTGACCAAGCTTCTACGACAACTTCTGAGTGCAGAACTC 893
Qy 541 TTCGAGATGCAACCAAGTTCAGCAAGTACTTCTGAGTTCAGAGTGTGCGGAAAGGT 600
Db 894 TTCGAGATGCAACCAAGTTCAGCAAGTACTTCTGAGTTCAGAGTGTGCGGAAAGGT 953
Qy 601 GGTTTTGGGAGTATGTCGCTGAGCTGCAAGGCTGAGGAGTGTATGCTGTAAG 660
Db 954 GGTTTTGGGAGTATGTCGCTGAGCTGCAAGGCTGAGGAGTGTATGCTGTAAG 1013
Qy 661 AAATCGCAAGAGCGCTGAAGAAAGAAAGTGGCGAGAGTGGCTCTCTTGGAAAAG 720
Db 1014 AAATCGCAAGAGCGCTGAAGAAAGAAAGTGGCGAGAGTGGCTCTCTTGGAAAAG 1073
Qy 721 GAAATCTTGGAGAGGTGACGAGCCCTTCTATGCTCTGCGCTATGCTTGGAGG 780

Db 1074 GAAATCTTGGAGAGGTGACGAGCCCTTCTATGCTCTCTGCGCTATGCTTGGAGC 1133
Qy 781 AAGACCCATCTCTGCTTGTGTCATGAGCCTGATGAATGGGGAGAGCCTCAAGTTCACATC 840
Db 1134 AAGACCCATCTCTGCTTGTGTCATGAGCCTGATGAATGGGGAGAGCCTCAAGTTCACATC 1193
Qy 841 TACAACGTGGGACGCGTGGCTGACATGAGCAGCGGTGATCTTTACTCGGCCAGATA 900
Db 1194 TACAACGTGGGACGCGTGGCTGACATGAGCAGCGGTGATCTTTACTCGGCCAGATA 1253
Qy 901 GCCTGTGGATGCTGCACTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
Db 1254 GCCTGTGGATGCTGCACTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313
Qy 961 AATGTGCTTCTGGATGACCTCGCAACTGCAAGTGTATCTGACCTGGGGCTGSCCTGGAG 1020
Db 1314 AATGTGCTTCTGGATGACCTCGCAACTGCAAGTGTATCTGACCTGGGGCTGSCCTGGAG 1373
Qy 1021 ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAACCAATGTTATATGCTCTGAG 1080
Db 1374 ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAACCAATGTTATATGCTCTGAG 1433
Qy 1081 ATCTTAATGGAAGGTAAAGTTATCTCTATCTCTGGAAGTGTGCTTGGCCATGCGATGCGAGC 1140
Db 1434 ATCTTAATGGAAGGTAAAGTTATCTCTATCTCTGGAAGTGTGCTTGGCCATGCGATGCGAGC 1493
Qy 1141 ATTTATGAAATGGTGTGCGACGAACCACTTCAAGAGTATCAAGAGAAAGGTCAAGTAAA 1200
Db 1494 ATTTATGAAATGGTGTGCGACGAACCACTTCAAGAGTATCAAGAGAAAGGTCAAGTAAA 1553
Qy 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGAGCATGATACTTCAACA 1260
Db 1554 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGAGCATGATACTTCAACA 1613
Qy 1261 GAGGACGCAAGATATTTGCGAGCTCTTCTGCTGAGAAACCAAGAGCAAGCTTAGGA 1320
Db 1614 GAGGACGCAAGATATTTGCGAGCTCTTCTGCTGAGAAACCAAGAGCAAGCTTAGGA 1673
Qy 1321 AGCAGAGAAAGTCTGATGATGCCAGGAAACATCATTTCTTTAAACCATCAACTTTCTCT 1380
Db 1674 AGCAGAGAAAGTCTGATGATGCCAGGAAACATCATTTCTTTAAACCATCAACTTTCTCT 1733
Qy 1381 CGCTGGAAGTGGCTTAATTTGAACCCCTTGTGCGAGACCCCTTCAAGTGGTATATGCC 1440
Db 1734 CGCTGGAAGTGGCTTAATTTGAACCCCTTGTGCGAGACCCCTTCAAGTGGTATATGCC 1793
Qy 1441 AAGACATCGCTGAATTTGATGATTTCTCTGAGGTTGCGGGGTGGAAATTTGATGACAAA 1500
Db 1794 AAGACATCGCTGAATTTGATGATTTCTCTGAGGTTGCGGGGTGGAAATTTGATGACAAA 1853
Qy 1501 GATAAGCAGTTCTTTCAAAACCTTTGCGACAGGTGCTGTTCTCTATAGCATGGCAGGAAGA 1560
Db 1854 GATAAGCAGTTCTTTCAAAACCTTTGCGACAGGTGCTGTTCTCTATAGCATGGCAGGAAGA 1913
Qy 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGTGAG 1620
Db 1914 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGTGAG 1973
Qy 1621 GAGGTAATTCATCCAAGTCTGGCGTGTGTTGTTATTG 1659
Db 1974 GAGGTAATTCATCCAAGTCTGGCGTGTGTTGTTATTG 2012

RESULT 7

US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases ar
; TITLE OF INVENTION: Polynucleotides

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; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-5

Query Match          99.8%; Score 1655.8; DB 14; Length 2249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTGGACATGGGGCCCTGGACAACCTGATCGCCAAACACCGCCTACCTGACGAGCCGG 60
DB 1 ATGGTGGACATGGGGCCCTGGACAACCTGATCGCCAAACACCGCCTACCTGACGAGCCGG 413
QY 61 AAGCCCTCGGACTGGACAGCAAGAGCTGACGCGCGCGCGCTAGCCTGCGCCCTGCC 120
DB 61 AAGCCCTCGGACTGGACAGCAAGAGCTGACGCGCGCGCGCTAGCCTGCGCCCTGCC 473
QY 121 GGGCTGACGGGCTGGCGGAGCTCGCCAGAGAGCTGCTCCGAACTTCCACAGCCTGTGT 180
DB 121 GGGCTGACGGGCTGGCGGAGCTCGCCAGAGAGCTGCTCCGAACTTCCACAGCCTGTGT 533
QY 181 GAGCAGCAGCCCATCGGTGCGCGCCTCTTCCGTGACTTCTTAGCCACAGTGCCACAGTTC 240
DB 181 GAGCAGCAGCCCATCGGTGCGCGCCTCTTCCGTGACTTCTTAGCCACAGTGCCACAGTTC 593
QY 241 CCAAGCGGCAACCTTCTAGACAGCTGACAGAGCTGGAGCTGGCGAGGAGGACCC 300
DB 241 CCAAGCGGCAACCTTCTAGAGAGCTGACAGAGCTGGAGCTGGCGAGGAGGAGCACC 653
QY 301 ACCAAGACAGCGCGCTGAGGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCGGG 360
DB 301 ACCAAGACAGCGCGCTGAGGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCGGG 713
QY 361 AACCCGCAACCTTCTCAGCAGCGCGGTGGCCACCAAGAGTCCAAAGCAGCCACCACTGAG 420
DB 361 AACCCGCAACCTTCTCAGCAGCGCGGTGGCCACCAAGAGTCCAAAGCAGCCACCACTGAG 773
QY 421 GAAGAGCGAGTGGCTGCAAGTGGCTGCGCAAGGCTGGAGGCTGGCCCTTCTTGAAG 480
DB 421 GAAGAGCGAGTGGCTGCAAGTGGCTGCGCAAGGCTGGAGGCTGGCCCTTCTTGAAG 833
QY 481 CAGCCCTTTAAGGATTTGCTGACACAGCGCTTCTACGACAAGTCTTCTGAGTGGAACTC 540
DB 481 CAGCCCTTTAAGGATTTGCTGACACAGCGCTTCTACGACAAGTCTTCTGAGTGGAACTC 893
QY 541 TTCGAGATGCAACCAAGTGTGACAAGTACTTCACTGAGTTTCAAGTCTCTGGGAAAGGT 600
DB 541 TTCGAGATGCAACCAAGTGTGACAAGTACTTCACTGAGTTTCAAGTCTCTGGGAAAGGT 953
QY 601 GGTTTTGGGAGTATGTGCGCTGACAGTGAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 660
DB 601 GGTTTTGGGAGTATGTGCGCTGACAGTGAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 1013
QY 661 AAATGGCAAGAACCGCTGAAGAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
DB 661 AAATGGCAAGAACCGCTGAAGAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG 1073
QY 721 GAAATCTTGGAAAGGTGACAGCCCTTTCATGTCTCTGGCCTATGCTTGGAGC 780
DB 721 GAAATCTTGGAAAGGTGACAGCCCTTTCATGTCTCTGGCCTATGCTTGGAGC 1133
QY 781 AAGACCCATCTCTGCTTGTGATGAGCCTGATGATGGGGAGAGCCTCAAGTCCACATC 840
DB 781 AAGACCCATCTCTGCTTGTGATGAGCCTGATGATGAGGGAGAGCCTCAAGTCCACATC 1193
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QY 841 TACAACGTGGGACGCGCTGGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 900
DB 1194 TACAACGTGGGACGCGCTGGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 1253
QY 901 GCCTGTGGATGCTGCACACCTCCATGAACCTCGGCACTCGTCTATCGGGACATGAAGCCTGAG 960
DB 1254 GCCTGTGGATGCTGCACACCTCCATGAACCTCGGCACTCGTCTATCGGGACATGAAGCCTGAG 1313
QY 961 AATGTGCTTCTGGATGACCTCGGCAACTGAGGTTATCTGACCTGGGCTGGCGTGGAG 1020
DB 1314 AATGTGCTTCTGGATGACCTCGGCAACTGAGGTTATCTGACCTGGGCTGGCGTGGAG 1373
QY 1021 ATGAAGGGTGGCAAGCGCCATCACACAGAGGCTGGAACCAATGTTATCATGCTCTCTGAG 1080
DB 1374 ATGAAGGGTGGCAAGCGCCATCACACAGAGGCTGGAACCAATGTTATCATGCTCTCTGAG 1433
QY 1081 ATCTTAATGGAAGAGGTAAGTTATTCCTATCTCTGGAAGCTGTTTGGCATGGGATGCAAGC 1140
DB 1434 ATCTTAATGGAAGAGGTAAGTTATTCCTATCTCTGGAAGCTGTTTGGCATGGGATGCAAGC 1493
QY 1141 ATTTATGAATGGTGTGCTGGACGAAACACCATTTCAAAGATTACAAGGAAAGGTCAGTAAA 1200
DB 1494 ATTTATGAATGGTGTGCTGGACGAAACACCATTTCAAAGATTACAAGGAAAGGTCAGTAAA 1553
QY 1201 GAGCATCTGAAGCAAGAAAGCTCTCAAGACGAGGTCAAATTCACAGCATGATACTTCAACA 1260
DB 1554 GAGCATCTGAAGCAAGAAAGCTCTCAAGACGAGGTCAAATTCACAGCATGATACTTCAACA 1613
QY 1261 GAGGAAGCAAGAAAGATTTTTCAGGCTCTTCTTGGCTAAGAAACAGAGCAACGCTTAGGA 1320
DB 1614 GAGGAAGCAAGAAAGATTTTTCAGGCTCTTCTTGGCTAAGAAACAGAGCAACGCTTAGGA 1673
QY 1321 AGCAGAGAAAGTCTGATGATGCCAGGAAACATCATTTCTTTAAACGATCAACTTTCCT 1380
DB 1674 AGCAGAGAAAGTCTGATGATGCCAGGAAACATCATTTCTTTAAACGATCAACTTTCCT 1733
QY 1381 CGCTGGAAGTGGCCCTAAATTTGAACCCCTTCTTGGCAGACCCCTTCAAGTGGTTTATGCC 1440
DB 1734 CGCTGGAAGTGGCCCTAAATTTGAACCCCTTCTTGGCAGACCCCTTCAAGTGGTTTATGCC 1793
QY 1441 AAAGACATCGCTGAAATGATGATTTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500
DB 1794 AAAGACATCGCTGAAATGATGATTTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1853
QY 1501 GATAAGCAGTCTTCAAAACTTTTGGCAGAGGCTGCTTCTATAGCATGCGCAGAGAGAA 1560
DB 1854 GATAAGCAGTCTTCAAAACTTTTGGCAGAGGCTGCTTCTATAGCATGCGCAGAGAGAA 1913
QY 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGTGAG 1620
DB 1914 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGTGAG 1973
QY 1621 GAGGTAATTCATCAAGCTGCGGCTGTGTTGTTATTG 1659
DB 1974 GAGGTAATTCATCAAGCTGCGGCTGTGTTGTTATTG 2012
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RESULT 8

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US-09-802-117-1
; Sequence 1, Application US/09802117
; Publication No. US20020042503A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444561 Human G-Coupled Protein Receptor Kinases and Polym
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-1

Query Match      99.8%; Score 1655.4; DB 9; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGGGACATGGGGCCCTGACAACTGATCGGCAACACCGCTACTCTGAGGCCCGG 60
DB 1 ATGTGGGACATGGGGCCCTGAGAACTGATCGGCAACACCGCTACTCTGAGGCCCGG 60
QY 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAAGCGCGCGGCTAGCTGCGCCCTGCC 120
DB 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAAGCGCGCGGCTAGCTGCGCCCTGCC 120
QY 121 GGGCTGCAAGGCTGCGCGGAGCTCCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
DB 121 GGGCTGCAAGGCTGCGCGGAGCTCCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
QY 181 GAGCAGAGCCCATCGTGCCTGCTTTCCTGAGCTTCTTCTGAGCAGCAGTGCACAGTTC 240
DB 181 GAGCAGAGCCCATCGTGCCTGCTTTCCTGAGCTTCTTCTGAGCAGCAGTGCACAGTTC 240
QY 241 CGCAGGCGGCAACCTTCTAGAGCAGTGCAGAACTGGAGCTGCGCGAGGAGGACCC 300
DB 241 CGCAGGCGGCAACCTTCTAGAGCAGTGCAGAACTGGAGCTGCGCGAGGAGGACCC 300
QY 301 ACCAAGACAGCGCTGCGAGGCTGTGGCCACTTGTGAGTGCCTGCTCCCGCGGG 360
DB 301 ACCAAGACAGCGCTGCGAGGCTGTGGCCACTTGTGAGTGCCTGCTCCCGCGGG 360
QY 361 AACCGCAACCTTCTCAGCAGCGCTGCGCCACCAAGTGCAGAGCAGCAGCAGTGCAG 420
DB 361 AACCGCAACCTTCTCAGCAGCGCTGCGCCACCAAGTGCAGAGCAGCAGCAGTGCAG 420
QY 421 GAAGAGCAGTGGCTGCAAGTGCAGTGCAGGCTGCGCAGGCTGAGCCATGGCTTCTTGAAG 480
DB 421 GAAGAGCAGTGGCTGCAAGTGCAGTGCAGGCTGCGCAGGCTGAGCCATGGCTTCTTGAAG 480
QY 481 CAGCCCTTTAAGATTTCTGACCAAGCGCTTCTACGCAAGTCTTCTGAGTGCAGAACTC 540
DB 481 CAGCCCTTTAAGATTTCTGACCAAGCGCTTCTACGCAAGTCTTCTGAGTGCAGAACTC 540
QY 541 TTCGAGATGCAACCAAGTGTGACAAAGTACTTCTCACTGAGTTCAGAGTCTGCGGAAAGGT 600
DB 541 TTCGAGATGCAACCAAGTGTGACAAAGTACTTCTCACTGAGTTCAGAGTCTGCGGAAAGGT 600
QY 601 GGTGTTGGGAGTATGTCCTGCTCAGTGGAACACCTGGGAAAGTATGATGCTGTAAG 660
DB 601 GGTGTTGGGAGTATGTCCTGCTCAGTGGAACACCTGGGAAAGTATGATGCTGTAAG 660
QY 661 AAATCGGCAAGAGCGCTGGAAGAAAGTGCAGAAAGTGCCTCTCTTGGAAAG 720
DB 661 AAATCGGCAAGAGCGCTGGAAGAAAGTGCAGAAAGTGCCTCTCTTGGAAAG 720
QY 721 GAAATCTTTGGAAGGTGACAGCCCTTTTCAATGCTCTCTGCGCTATGCTTTCAGAGC 780
DB 721 GAAATCTTTGGAAGGTGACAGCCCTTTTCAATGCTCTCTGCGCTATGCTTTCAGAGC 780
QY 781 AAGACCCATCTCTGCTTGTATGAGCTGATGAGTGGGGAGAGCTCAAGTTCACATC 840
DB 781 AAGACCCATCTCTGCTTGTATGAGCTGATGAGTGGGGAGAGCTCAAGTTCACATC 840
QY 841 TACAACGTGGGACCGCTGGCCTGGACATGAGCGGGTATCTTTTACTCGGCCAGATA 900
DB 841 TACAACGTGGGACCGCTGGCCTGGACATGAGCGGGTATCTTTTACTCGGCCAGATA 900
QY 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCTGCTATCGGGACATGAAGCCTGAG 960
DB 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCTGCTATCGGGACATGAAGCCTGAG 960
QY 961 AATGTGCTTCTGATGACCTCGGCAACTGCAAGTTTATCTGACCTGGGGCTGCCCGTGGAG 1020
DB 961 AATGTGCTTCTGATGACCTCGGCAACTGCAAGTTTATCTGACCTGGGGCTGCCCGTGGAG 1020
QY 1021 ATGAAGGTGCAAGGCCCATCACCCAGAGGGCTGGAACAATGGTTTACATGCTCTCTGAG 1080
DB 1021 ATGAAGGTGCAAGGCCCATCACCCAGAGGGCTGGAACAATGGTTTACATGCTCTCTGAG 1080
QY 1081 ATCTTAATGGAAGGTAAGTTATTTCTTATCTCTGGAAGTGGTTTGGCCATGGGATGCAGC 1140
DB 1081 ATCTTAATGGAAGGTAAGTTATTTCTTATCTCTGGAAGTGGTTTGGCCATGGGATGCAGC 1140
QY 1141 ATTTATGAAATGTTGCTGGAAGCAACCACTTCAAGAGTTTACAAGAAAAGGTTCAGTAAA 1200
DB 1141 ATTTATGAAATGTTGCTGGAAGCAACCACTTCAAGAGTTTACAAGAAAAGGTTCAGTAAA 1200
QY 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATTCACAGCATGATTAATCTTACA 1260
DB 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGTCAAAATTCACAGCATGATTAATCTTACA 1260
QY 1261 GAGGAGCAAGAGATATTTGCAAGGCTTCTTGGCTAAGAACCCAGAGCAAGCCTTAGGA 1320
DB 1261 GAGGAGCAAGAGATATTTGCAAGGCTTCTTGGCTAAGAACCCAGAGCAAGCCTTAGGA 1320
QY 1321 AGCAGAGAAAAGTCTGATGATCCCAAGGAAAATCATTTCTTTAAAACGATCAACTTTCTCT 1380
DB 1321 AGCAGAGAAAAGTCTGATGATCCCAAGGAAAATCATTTCTTTAAAACGATCAACTTTCTCT 1380
QY 1381 CGCTGGAAGTGGCTTAATTAAGCCCAATTTGTCAGAGCCCTTCAAGTGGTTTATGCTTATGCC 1440
DB 1381 CGCTGGAAGTGGCTTAATTAAGCCCAATTTGTCAGAGCCCTTCAAGTGGTTTATGCTTATGCC 1440
QY 1441 AAAGCATCGCTGAAATGATGATTTCTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500
DB 1441 AAAGCATCGCTGAAATGATGATTTCTCTGAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1500
QY 1501 GATAGCAGTCTTCAAAAACCTTTGCGACAGTGTCTTCTATAGCATGGCAGGAAGAA 1560
DB 1501 GATAGCAGTCTTCAAAAACCTTTGCGACAGTGTCTTCTATAGCATGGCAGGAAGAA 1560
QY 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACCGGTTGTGAG 1620
DB 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACCGGTTGTGAG 1620
QY 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTTGTATTG 1659
DB 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTTGTATTG 1659

RESULT 9
US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases an
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIORITY FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIORITY FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
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ORGANISM: homo sapiens
US-10-217-745-1

Query Match 99.8%; Score 1655.4; DB 14; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGCTGGACATGGGGCCCTGACAACTGATCGCAACACCGCTACTGCGAGCCCGG	60
DB	1	ATGCTGGACATGGGGCCCTGAYAACTGATCGCAACACCGCTACTGCGAGCCCGG	60
QY	61	AAGCCCTCGGACTGCGACAGCAAAAGAGTGCAGCGCGCGCGTAGCCTGCGCC	120
DB	61	AAGCCCTCGGACTGCGACAGCAAAAGAGTGCAGCGCGCGCGTAGCCTGCGCC	120
QY	121	GGCTGCGAGGCTGCGCGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCCTGT	180
DB	121	GGCTGCGAGGCTGCGCGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCCTGT	180
QY	181	GAGCAGCAGCCCATCGCTCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC	240
DB	181	GAGCAGCAGCCCATCGCTCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC	240
QY	241	CGCAGCGCGCAACTTCTTAGAGACGTGCAGAACTGGAGCTGGCGAGGAGGCC	300
DB	241	CGCAGCGCGCAACTTCTTAGAGACGTGCAGAACTGGAGCTGGCGAGGAGGCC	300
QY	301	ACCAAGACAGCGCTGCGAGGCTGCGGCTGCTGCGAGTGCCTGCGCCCGGG	360
DB	301	ACCAAGACAGCGCTGCGAGGCTGCGGCTGCTGCGAGTGCCTGCGCCCGGG	360
QY	361	AACCCGCAACCTTCTCAGCAGCGCTGCGCAAGTGCAGAGCAGCCACACTGAG	420
DB	361	AACCCGCAACCTTCTCAGCAGCGCTGCGCAAGTGCAGAGCAGCCACACTGAG	420
QY	421	GAAGAGCGAGTGGCTGCGAGTGCAGTGCAGAGCTGAGGCGCATGGCTTTCTTGAAG	480
DB	421	GAAGAGCGAGTGGCTGCGAGTGCAGTGCAGAGCTGAGGCGCATGGCTTTCTTGAAG	480
QY	481	CAGCCCTTTAAGGATTTGTCAGCAGCGCTTCTACGACAGTTCCTCAGTGGAACTC	540
DB	481	CAGCCCTTTAAGGATTTGTCAGCAGCGCTTCTACGACAGTTCCTCAGTGGAACTC	540
QY	541	TTGAGATGCAACACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAG	600
DB	541	TTGAGATGCAACACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAG	600
QY	601	GGTTTGGGAGGTATGTCCTCAGGTGAAACACCTGGGAAGATGTATGCTGTAAAG	660
DB	601	GGTTTGGGAGGTATGTCCTCAGGTGAAACACCTGGGAAGATGTATGCTGTAAAG	660
QY	661	AAACTGGACAAGCGCTGAAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG	720
DB	661	AAACTGGACAAGCGCTGAAGAAAGTGGCGAGAGATGGCTCTCTTGGAAAG	720
QY	721	GAAATCTTTGGAAGGTGACAGCCCTTTCAATGCTCTGCGCTATGCTTTGAGAGC	780
DB	721	GAAATCTTTGGAAGGTGACAGCCCTTTCAATGCTCTGCGCTATGCTTTGAGAGC	780
QY	781	AAGACCATCTGCTGCTGTCATGAGCTGATGAATGGGGAGAGCTCAAGTTCACATC	840
DB	781	AAGACCATCTGCTGCTGTCATGAGCTGATGAATGGGGAGAGCTCAAGTTCACATC	840
QY	841	TACACGTGGGACCGCTGGCTGACATGAGCGGGTATCTTTTACTCGGCCAGATA	900
DB	841	TACACGTGGGACCGCTGGCTGACATGAGCGGGTATCTTTTACTCGGCCAGATA	900
QY	901	GCCTGTGGATGCTGCACCTCCAGACTCGGCATCGTCTATCGGGACATGAAGCTGAG	960
DB	901	GCCTGTGGATGCTGCACCTCCAGACTCGGCATCGTCTATCGGGACATGAAGCTGAG	960
QY	961	AATGTGCTTCTGGATGACTCGGCACTGCAGTTATCTGACCTGGGCTGGCGTGGAG	1020
DB	961	AATGTGCTTCTGGATGACTCGGCACTGCAGTTATCTGACCTGGGCTGGCGTGGAG	1020

Query Match 99.7%; Score 1654.2; DB 9; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;

RESULT 10

US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL000636DIV

CURRENT APPLICATION NUMBER: US/09/964,469

CURRENT FILING DATE: 2001-09-28

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: 09/738,894

PRIOR FILING DATE: 2000-12-18

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1662

TYPE: DNA

ORGANISM: Human

US-09-964-469-1

[illegible]

Db	1081	ATCCTAATGGAAAGGTAAAGTTATTCCTATCTGTGTGGACGTGGTTTGGCATGGGATGCAGC	11440
Qy	1141	ATTATGAAATCGTGTCTGGACGAAACCAATTCAAAGATTTACAAGGAAAGGTCAGTAAA	1200
Db	1141	ATTATGAAATCGTGTCTGGACGAAACCAATTCAAAGATTTACAAGGAAAGGTCAGTAAA	1200
Qy	1201	GAGGATCTGAAGCAAAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATACTTCACA	1260
Db	1201	GAGGATCTGAAGCAAAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATACTTCACA	1260
Qy	1261	GAGGAACAAAAGATATTTCGAGGCTCTCTTGGCTTAAGAAACCGAGCAACGCTTAGGA	1320
Db	1261	GAGGAACAAAAGATATTTCGAGGCTCTCTTGGCTTAAGAAACCGAGCAACGCTTAGGA	1320
Qy	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT	1380
Db	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT	1380
Qy	1381	CGCTGGAAGCTGGCCCTAAATTGAAACCCCAATTTGTCAGACGACCTTCAGTGGTTTATGCC	1440
Db	1381	CGCTGGAAGCTGGCCCTAAATTGAAACCCCAATTTGTCAGACGACCTTCAGTGGTTTATGCC	1440
Qy	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTCTGGGGGTGGAAATTTGATGACAAA	1500
Db	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTCTGGGGGTGGAAATTTGATGACAAA	1500
Qy	1501	GATAAGCAGTTCTTCAAAAACCTTTGGCAGAGTGCTGTTCCTATAGCATGGCAGGAGAA	1560
Db	1501	GATAAGCAGTTCTTCAAAAACCTTTGGCAGAGTGCTGTTCCTATAGCATGGCAGGAGAA	1560
Qy	1561	ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAAGACCTACGGGTTCTGTAG	1620
Db	1561	ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAAGACCTACGGGTTCTGTAG	1620
Qy	1621	GAGGGTAATTCATCCAAGTCTGGCGTGTGTTGTTATTG	1659
Db	1621	GAGGGTAATTCATCCAAGTCTGGCGTGTGTTGTTATTG	1659

RESULT 12
US-10-072-012-273
; Sequence 273, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zertusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsebrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nuc
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/07
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-273

Query Match          95.8%; Score 1589.8; DB 17; Length 1701;
Best Local Similarity 98.6%; Pred No. 0;
Matches 1642; Conservative 0; Mismatches 2; Indels 21; Gaps 3;

QY 1 ATGTGGACATGGGGCCCTGACAACTGTATCGCCAAACACCGCCTACCTGCGAGCCCGG 60
DB 19 ATGTGGACATGGGGCCCTGACAACTGTATCGCCAAACACCGCCTACCTGCGAGCCCGG 78
QY 61 AAGCCCTGGACTGGACAGCAAGAGCTGACGGCGGCGGTAGCCCTGCGCCCTGCC 120
DB 79 AAGCCCTGGACTGGACAGCAAGAGCTGACGGCGGCGGTAGCCCTGCGCCCTGCC 138
QY 121 GGGCTGCGAGGGCTGCGCGAGCTCCGCGAGAGCTGCTCCGAACTTCCACAGCCTGTGT 180
DB 139 GGGCTGCGAGGGCTGCGCGAGCTCCGCGAGAGCTGCTCCGAACTTCCACAGCCTGTGT 198
QY 181 GAGCAGCAGCCCATCGCTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCCCACTTC 240
DB 199 GAGCAGCAGCCCATCGCTGCGCGCTCTTCCGTGACTTCTAGCCACAGTGCCCACTTC 258
QY 241 CGCAAGCGGCAACTTCTTAGAGACCTGTCAGAACTGGAGCTGGCGAGGAGGAGCC 300
DB 259 CGCAAGCGGCAACTTCTTAGAGACCTGTCAGAACTGGAGCTGGCGAGGAGGAGCC 318
QY 301 ACCAAGACAGCGCTGCGAGGGCTGGTGGCACTTGTGCGAGTGCCCTGCCCGGGG 360
DB 319 ACCAAGACAGCGCTGCGAGGGCTGGTGGCACTTGTGCGAGTGCCCTGCCCGGGG 378
QY 361 AACCCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGCCAGCAGCCCACTGAG 420
DB 379 AACCCGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGCCAGCAGCCCACTGAG 438
QY 421 GAAGAGCAGTGCTGCAAGTACGCTGGCGCAAGGCTGAGGCGCATGGCTTTTTCGAAGAG 480
DB 439 GAAGAGCAGTGCTGCAAGTACGCTGGCGCAAGGCTGAGGCGCATGGCTTTTTCGAAGAG 498
QY 481 CAGCCCTTTAAGGATTTGTGACAGCGCTTCTACGCAAGTTCCTGCGAGTGGAACTC 540
DB 499 CAGCCCTTTAAGGATTTGTGACAGCGCTTCTACGCAAGTTCCTGCGAGTGGAACTC 558
QY 541 TTCGAGATGCAACAGTGTGACAGTACTTCACTGAGTTCAGAGTGTGCGGAAAGT 600
DB 559 TTCGAGATGCAACAGTGTGACAGTACTTCACTGAGTTCAGAGTGTGCGGAAAGT 618
QY 601 GGTTTTGGGAGGTATGTGCCGTCCAGGTGAAACACCTGGGAAAGATGTATGCCCTGTAG 660
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RESULT 13
US-09-802-117-3

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DB 619 GGTTTTGGGAGGTA-----AAAAACACTGGGAAGATGTATGCCCTGTAG 663
QY 661 AAACCTGGACAAGACGGCTGAAGAAGAAAGGTGCGGAAGATGGCTCTCTTTGGAAG 720
DB 664 AAACCTGGACAAGACGGCTGAAGAAGAAAGGTGCGGAAGATGGCTCTCTTTGGAAG 723
QY 721 GAAATCTTTGGAGAAGGTGACAGCCCTTTTCATTTGTCTCTGCGCTATGCCCTTGAGAGC 780
DB 724 GAAATCTTTGGAGAAGGTGACAGCCCTTTTCATTTGTCTCTGCGCTATGCCCTTGAGAGC 783
QY 781 AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC 840
DB 784 AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC 843
QY 841 TACAACTGGGCAAGCGCTGGCTGGACATGAGCCGGTGTATCTTTACTCGGCCCAAGATA 900
DB 844 TACAACTGGGCAAGCGCTGGCTGGACATGAGCCGGTGTATCTTTACTCGGCCCAAGATA 903
QY 901 GCCTGTGGATGCTGCACCTCTCACTGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
DB 904 GCCTGTGGATGCTGCACCTCTCACTGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 963
QY 961 AATGTGCTTCTGGATGACCTCGGCAACTGACGTTTATCTGACCTGCGGCTGCGCTGGAG 1020
DB 964 AATGTGCTTCTGGATGACCTCGGCAACTGACGTTTATCTGACCTGCGGCTGCGCTGGAG 1023
QY 1021 ATGAAGGCTGGCAAGCCCATCACCCAGAG---GGCTGGAACCAATGCTTACATGGCTCCT 1077
DB 1024 ATGAAGGCTGGCAAGCCCATCACCCAGAGGCGCTGGAACCAATGCTTACATGGCTCCT 1083
QY 1078 GAGATCTTAATGGAAAAAGGTAACTTCTATCTCTGTGGACTGTTTGGCCATGGGATGC 1137
DB 1084 GAGATCTTAATGGAAAAAGGTAACTTCTATCTCTGTGGACTGTTTGGCCATGGGATGC 1143
QY 1138 AGCATTATGAATGGTTGCTGGAGCAACCAATCAAGATTACAAGAAAGGTCACT 1197
DB 1144 AGCATTATGAATGGTTGCTGGAGCAACCAATCAAGATTACAAGAAAGGTCACT 1203
QY 1198 AAAGAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATAACTTC 1257
DB 1204 AAAGAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATAACTTC 1263
QY 1258 ACAGAGGAAGCAAGATATTTGCAAGGCTCTTCTTGGCTTAAGAAACCAAGAGCAAGCTTA 1317
DB 1264 ACAGAGGAAGCAAGATATTTGCAAGGCTCTTCTTGGCTTAAGAAACCAAGAGCAAGCTTA 1323
QY 1318 GGAAGC---AGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAAC 1374
DB 1324 GGAAGCAGGAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAAC 1383
QY 1375 TTTCTCGCTGGAGAGCTGGCTTAATTCGAACCCCATTTGTGCCAGAGCCCTTCAGTGGTT 1434
DB 1384 TTTCTCGCTGGAGAGCTGGCTTAATTCGAACCCCATTTGTGCCAGAGCCCTTCAGTGGTT 1443
QY 1435 TATGCCAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTGAT 1494
DB 1444 TATGCCAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTGAT 1503
QY 1495 GACAAAGATGAAGAGTCTTCTCAAAAACCTTTGGGACAGTGTCTTCTATAGCATGGCAG 1554
DB 1504 GACAAAGATGAAGAGTCTTCTCAAAAACCTTTGGGACAGTGTCTTCTATAGCATGGCAG 1563
QY 1555 GAAGAAATTAAGAAACGGGACTGTTTCAGGAACCTGAATGACCCCAACAGACCTACGGGT 1614
DB 1564 GAAGAAATTAAGAAACGGGACTGTTTCAGGAACCTGAATGACCCCAACAGACCTACGGGT 1623
QY 1615 TGTGAGGAGGTAAATTCATCAAGTCTGCGCTGTCTTTGTTATTG 1659
DB 1624 TGTGAGGAGGTAAATTCATCAAGTCTGCGCTGTCTTTGTTATTG 1668
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; Sequence 3, Application US/09802117
; Publication No. US20020042503A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444561 Human G-Coupled Protein Receptor Kinases and Polynu
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3

Query Match      63.1%; Score 1046.8; DB 9; Length 1062;
Best Local Similarity 99.8%; Pred. No. 2.8e-307;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGGACATGGGGGCGCTGGACAACTGATCGCAACACCGCTTACTGCGAGCCCGG 60
DB 1 ATGTGGACATGGGGGCGCTGGACAACTGATCGCAACACCGCTTACTGCGAGCCCGG 60
QY 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGGCTGAGCTGGCCCTGCC 120
DB 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGGCTGAGCTGGCCCTGCC 120
QY 121 GGGCTGACGGCTGCGCGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCTGTG 180
DB 121 GGGCTGACGGCTGCGCGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCTGTG 180
QY 181 GAGCAGCAGCCCATCGGTCGCGCGCTCTTCCTGATCTTCCAGCAGCTGCGACAGTTC 240
DB 181 GAGCAGCAGCCCATCGGTCGCGCGCTCTTCCTGATCTTCCAGCAGCTGCGACAGTTC 240
QY 241 CGCAAGCGGGCAACCTTCTAGAGACGTGCGAAGCTGCGAGCTGGCGAGGAGGCC 300
DB 241 CGCAAGCGGGCAACCTTCTAGAGACGTGCGAAGCTGCGAGCTGGCGAGGAGGCC 300
QY 301 ACCAAGACAGCGCGCTGCGAGGCTGCGGCACTTGTGCGAGTGCCTGCGCCCGGG 360
DB 301 ACCAAGACAGCGCGCTGCGAGGCTGCGGCACTTGTGCGAGTGCCTGCGCCCGGG 360
QY 361 AACC CGCAACCTTCTCTCAGCGAGCGCTGGCCACCAAGTGCACAGCAGCCACCACTGAG 420
DB 361 AACC CGCAACCTTCTCTCAGCGAGCGCTGGCCACCAAGTGCACAGCAGCCACCACTGAG 420
QY 421 GAAGAGCGAGTGGCTGCGAGTGAACGCTGCGCAAGGCTGAGGCCATCGCTTTCTTGAAG 480
DB 421 GAAGAGCGAGTGGCTGCGAGTGAACGCTGCGCAAGGCTGAGGCCATCGCTTTCTTGAAG 480
QY 481 CAGCCCTTTAAGATTTCGTGACCAAGCGCTTCTACGACAGTTCCTGAGTGGAACTC 540
DB 481 CAGCCCTTTAAGATTTCGTGACCAAGCGCTTCTACGACAGTTCCTGAGTGGAACTC 540
QY 541 TTCGAGATGCAACACAGTGTGACAAAGTACTTCTACTGATTCAGAGTGTGCGGGAAGGT 600
DB 541 TTCGAGATGCAACACAGTGTGACAAAGTACTTCTACTGATTCAGAGTGTGCGGGAAGGT 600
QY 601 GGTTCCTGGAGTATGTCCTGCGTCAAGTGAAGAACTGCGGAAAGTATGATGCTGTAAG 660
DB 601 GGTTCCTGGAGTATGTCCTGCGTCAAGTGAAGAACTGCGGAAAGTATGATGCTGTAAG 660
QY 661 AAATGGAAGAAGCGGCTGAAGAAAGAGTGGCGAAGAGTGGCTCTCTTTGGAAG 720
DB 661 AAATGGAAGAAGCGGCTGAAGAAAGAGTGGCGAAGAGTGGCTCTCTTTGGAAG 720
```

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QY 721 GAAATCTTGAGAAAGTCAAGAGCCCTTTCAATCTCTCTGCGCTATGCTTTGAGAGC 780
DB 721 GAAATCTTGAGAAAGTCAAGAGCCCTTTCAATCTCTCTGCGCTATGCTTTGAGAGC 780
QY 781 AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGAGACCTCAAGTTCACATC 840
DB 781 AAGACCCATCTCTGCTTGTATGAGCTGATGATGGGGAGACCTCAAGTTCACATC 840
QY 841 TACAACGTGGGACGCGTGGCTGGACATGAGCCGGTGTATCTTACTCGGCCAGATA 900
DB 841 TACAACGTGGGACGCGTGGCTGGACATGAGCCGGTGTATCTTACTCGGCCAGATA 900
QY 901 GCCTGTGGATGTGCGACATCCATGAACCTGCGATCGTGTATCGGACATGAAGCCTGAG 960
DB 901 GCCTGTGGATGTGCGACATCCATGAACCTGCGATCGTGTATCGGACATGAAGCCTGAG 960
QY 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTGTATCTGACCTGGGCTGGCGTGGAG 1020
DB 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTGTATCTGACCTGGGCTGGCGTGGAG 1020
QY 1021 ATGAAGGTGGCAAGCCCATCACCAGAGG 1050
DB 1021 ATGAAGGTGGCAAGCCCATCACCAGAGG 1050
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RESULT 14

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US-10-217-745-3
; Sequence 3, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases an
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-3
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Best Local Similarity 99.8%; Pred. No. 2.8e-307;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 121 GGGCTGACGGCTGCGCGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCTGTG 180
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QY 901 GCCTGTGGATGCTGCACCTCCATCACTCGCATCGTCTATCGGACATGAAGCTGAG 960
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; Sequence 3, Application US/09964469
; Patent No. US2002034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3
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Best Local Similarity 96.8%; Pred. No. 8.5e-176;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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Db 2616 TTCGAGATGCAACCAAGTGTGACCAAGTACTTCACTGAGTTCAGAGTGTGCGGAAAGT 2675
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Db 2676 GGTTCGAGAGTATGTGCGCTCCAGGTGAAAGTGTATGAAGGTGAAGCAT 2726
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Job time : 2179.58 secs

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GenCore version 5.1.6
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Run on: May 11, 2005, 00:47:58 ; Search time 258 Seconds
(without alignments)
3507.213 Million cell updates/sec

Title: US-10-044-205A-2

Perfect score: 2889

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2876	99.6	1662	3	US-09-738-894A-1
6	2876	99.6	1662	4	US-09-964-469-1
7	1801	62.3	1062	3	US-09-802-117-3
8	1801	62.3	1062	4	US-10-217-745-3
9	1528	52.9	3651	3	US-09-738-894A-3
10	1528	52.9	3651	4	US-09-964-469-3
11	1280.5	44.3	2113	4	US-09-614-748A-7
12	1252.5	43.4	2511	4	US-09-417-197-60

13	1252.5	43.4	2529	4	US-09-417-197-42	Sequence 42, Appl
14	1252.5	43.4	2557	4	US-09-016-434-1298	Sequence 1298, Ap
15	1250.5	43.3	1975	4	US-09-614-748A-9	Sequence 9, Appli
16	1243.5	43.0	2017	4	US-09-614-748A-8	Sequence 8, Appli
17	1240	42.9	2848	3	US-08-464-954A-2	Sequence 2, Appli
18	1238	42.9	2204	1	US-08-221-817-12	Sequence 12, Appl
19	1238	42.9	2204	1	US-08-454-439-12	Sequence 12, Appl
20	1238	42.9	2204	5	PCT-US94-10487-12	Sequence 12, Appl
21	1236.5	42.8	2557	3	US-08-464-954A-1	Sequence 1, Appli
22	1210.5	41.9	1879	4	US-09-614-748A-10	Sequence 10, Appl
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32	725.5	25.1	2362	4	US-09-620-312D-273	Sequence 273, App
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36	509.5	17.6	2396	4	US-09-949-016-1735	Sequence 1735, Ap
37	507	17.5	3255	4	US-09-016-434-1471	Sequence 1471, Ap
38	507	17.5	6102	4	US-09-949-016-2007	Sequence 2007, Ap
39	493	17.1	2705	4	US-09-949-016-839	Sequence 839, App
40	493	17.1	2715	4	US-09-949-016-1959	Sequence 1959, Ap
41	493	17.1	2754	3	US-09-429-322-3	Sequence 3, Appli
42	473.5	16.4	2274	4	US-09-772-647-3	Sequence 3, Appli
43	473	16.4	2499	4	US-09-949-016-5704	Sequence 5704, Ap
44	472.5	16.4	2324	4	US-09-190-976B-6	Sequence 6, Appli
45	469	16.2	2104	3	US-09-313-930-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-802-117-1
; Sequence 1, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456 Human G-Coupled Protein Receptor Kinases and Polyn
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802.117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-1

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Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
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US-10-044-205A-2 (1-553) x US-09-802-117-1 (1-1662)

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RESULT 2

US-10-217-745-1

; Sequence 1, Application US/10217745

; Patent No. 6838275

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wilganowski, Nathaniel L.

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and

; TITLE OF INVENTION: Polynucleotides

; TITLE OF INVENTION: Encoding the Same

; FILE REFERENCE: LEX-0147-USA

; CURRENT APPLICATION NUMBER: US/10/217,745

; CURRENT FILING DATE: 2002-08-12

; PRIOR APPLICATION NUMBER: US/09/802,117

; PRIOR FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1662

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-217-745-1

Alignment Scores:

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Score:	2883.00	Matches:	552
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.75%	Indels:	0
DB:	4	Gaps:	0

US-10-044-205A-2 (1-553) x US-10-217-745-1 (1-1662)

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Db 601 GGTTTGGGAGGTATGTGCGCTCCAGGTGAAACACTGGGAGAGTATGTGCTGTAAAG 660
Qy 221 LysLeuAspLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
Db 661 AAATCGGACAAAGACGGCTCAAGAAGAAGGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Qy 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db 721 GAATCTTGGAGAGTGCAGCGCTTCTATGTCTCTCTGGCCCTATGCCCTTTGAGAGC 780
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuPheHisIle 280
Db 781 AAGACCCATCTCTGCTTGTCTATGAGCTGATGAATGGGGAGACCTCAAGTTCCACATC 840
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACGTGGGACCGCGTGGCTGACATGAGCGGGGTATCTTTTACTCGCGCCAGATA 900
Qy 301 AlaCysGlyMetLeuHisLeuGluGlyIleValTyrArgAspMetLysProGlu 320
Db 901 GCCTGTGGATGCTGCATCTCATGACTCGCATCTGCTATCGGACATGAAGCCTGAG 960
Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db 961 AATGTGCTCTGATGACCTCGCAACTGCAGGTTATCTGACCTGGGCGCTGGCGTGGAG 1020
Qy 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db 1021 ATGAAGGGTGGCAAGCCCATCCAGAGGGGTGGAACCAATGGTTACATGGCTCCTCAG 1080
Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
Db 1081 ATCTTAATGGAAAGGTAAGTTATTCTCTATCTGTGGACTGGTTTGGCATGGGATGACG 1140
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Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
Db 1141 ATTTATGAATGGTGTGTCGACGAACACCATTTCAAAGATTACAAGGAAAGGTTCAGTAAA 1200
Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAGACGAGGTCAAAATTCAGCATGATAACTTCACA 1260
Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
Db 1261 GAGGAAGCAAAAGATATTTGCGAGCTCTTCTTGGCTAAGAAACACGAGCAACGCTTAGGA 1320
Qy 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
Db 1321 AGCAGAGAAAAGTCTGATGATCCCGAGGAAACATCATTTCTTTAAACCATCAACTTCTCT 1380
Qy 461 ArgLeuGluAlaGlyLeuLeuGluProPheValProAspProSerValValTyrAla 480
Db 1381 CGCTTGGAGTGGCTTAATTTGAACCCCATTTGTGCCAGACCTTCACTGTTTATGTC 1440
Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db 1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGTGGAATTTGATGACAAA 1500
Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
Db 1501 GATAAGCAGTTCTTTCAAAACCTTTTGCAGACAGTCTGTTCTTATAGCATGCGAGGAAGA 1560
Qy 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGTAATTCATCCAAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 3
US-09-802-117-5
; Sequence 5, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Alignment Scores:
Pred. No.: 0 Length: 2249
Score: 2893.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 3 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-5 (1-2249)

Qy 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 354 ATGTGGACATGGGGGCGCTCGAACCTGATGCCAACACCGCTACCTGAGCGCCGG 413
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21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
414 AAGCCCTCGGACTGGCAGCAAGAGCTGCAGCGGGCGGCTAGCCTGGCCCTGCC 473
41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLysCys 60
474 GGGCTGCAGGGCTGGCGGAGCTCCGCCAGAGCTGCTCCCTGAACCTCCACAGCCTGTGT 533
61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
534 GAGCAGCAGCCATCGCTGGCGGCTCTTCCTCGTGAATTCCTTAGCCACAGTGCACAGTTC 593
81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTTPGluLeuAlaGluGluGlyPro 100
594 CGCAGGCGGCAACCTCTCTAGAGAGCTGCAGAACTGGGAGCTGGCCGAGAGGGACCC 653
101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
654 ACCAAGACAGCGGCTGCAGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCGGG 713
121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
714 AACCGCAACCTCTCTCAGCGAGCGCTGCCCAAGTGCAGAGCAGCCACCACTGAG 773
141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
774 GAAGACGAGTGGCTGCAGTACGCTGGCCAGGCTGAGGCCATGGCTTTCTTGAAGAG 833
161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
834 CAGCCCTTTAGGATTTCTGTACCAAGCGCTTCTACGACAAGTTTCTGCAGTGGAACTC 893
181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
894 TTCGAGATGCAACACCAAGTGTACAGAACTTCTCACTGAGTTTCAGAGTGTGGGAAAGGT 953
201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
954 GGTTCGGGAGTATGTGCGCTCCAGGTGAANAACACTGGGAAGTGTATGCTGTAA 1013
221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyLysMetAlaLeuLeuLys 240
1014 AAATGGCAAGAGCGGCTGAAGAAGAAAGTGGCGAGAGATGGCTCTCTTGGANAAG 1073
241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
1074 GAAATCTTGGAGAGTCAAGAGCCTTCTCATGTCTCTGGCTATGCCCTTTCAGAGC 1133
261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLysPheHisIle 280
1134 AGACCCATCTCTGCTTGTATGAGCCTGATGATGGGGAGACCTCAAGTTCCACATC 1193
281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerIleGlnIle 300
1194 TACAACGTGGCAGCGCTGGCCATGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 1253
301 AlaCysGlyMetLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
1254 GCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGACATGAGGCTGAG 1313
321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuAlaValGlu 340
1314 AATGTGCTTCTGATGACCTCGCAACTCGAGTTATCTGACCTGGGGCTGGCGGTGAG 1373
341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
1374 ATGAGGGTGGCAAGCCCATCCAGAGGGCTGGAAACCAATGTTTACATGGCTCTCTGAG 1433
361 IleLeuMetGluLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
1434 ATCTTAATGGAAGAGTAGTATTCCTATCTGTGAGCTGGTTTCCTGAGTGCAGC 1493
381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400

1494 ATTTATCAATGCTGTCTGGACCAACCACTTCAAGGAAAAGGTCACTATAA 1553
401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
1554 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTCAATTCAGCATGATTAATCTTCA 1613
421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
1614 GAGGAGCAAAAGATATTTGCAGGCTCTTCTGGCTAAGAAACAGAGCAACGCTTAGGA 1673
441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
1674 AGCAGAGAAAAGTCTGATGATCCAGGAAACATCTTCTTTAAACGATCACTTTTCT 1733
461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
1734 CGCTGGAAAGTGGCTTAAATTTGAACCCCAATTTGTGCCAGACCTTCAGTGGTTATGCC 1793
481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
1794 AAAGACATCGCTGAAATTTGATTTCTCTGAGGTTCCGGGGGTGGAATTTGATGACAAA 1853
501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTyrGlnGluGlu 520
1854 GATAAGCAGTCTCTCAAAAACTTTGCCAGAGGTCTGTTCTCTATAGCATGGCAGGAAGA 1913
521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
1914 ATTTAGAAACGGGACCTGTTTGAAGAACTGATGACCCCAACAGACCTACGGGTGTGAG 1973
541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
1974 GAGGTAATTCATCAAGTCTGGCTGTGTTGTTATTG 2012

RESULT 4

US-10-217-745-5

; Sequence 5, Application US/10217745

; Patent No. 6838275

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wilganowski, Nathaniel L.

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and

; TITLE OF INVENTION: Polynucleotides

; TITLE OF INVENTION: Encoding the Same

; FILE REFERENCE: LEX-0147-USA

; CURRENT APPLICATION NUMBER: US/10/217,745

; CURRENT FILING DATE: 2002-08-12

; PRIOR APPLICATION NUMBER: US/09/802,117

; PRIOR FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 2249

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-217-745-5

Alignment Scores:

Pred. No.:	0	Length:	2249
Score:	2883.00	Matches:	552
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.79%	Indels:	0
DB:	4	Gaps:	0

US-10-044-205A-2 (1-553) x US-10-217-745-5 (1-2249)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrIleuGlnAlaArg 20
DB 354 ATGGTGGACATGGGGGCGCTCGACAACTGATCGCAACACCGCCTACCTGCGAGCCCGG 413

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QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
DB 414 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGCGGTAGCTGGCCCTGGCCC 473
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 474 GGGCTGCAGGGCTGCGCGAGCTCGCCAGAGCTGTCCCTGAACTTCCACAGCCCTGTGT 533
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 534 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCTGAGCTTCCTAGCCACAGTGCACAGTTC 593
QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGluPro 100
DB 594 CGCAAGCGCGCAACCTCTCTAGAGACGTCGAGAACTGGGAGCTGGCGAGGAGGAGCC 653
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 654 ACCAAGACAGCGCGCTGAGGGGTGTGGCCACTTGTGGAGTGGCCCTGGCCCGGG 713
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 714 AACCGCAACCTCTCTCAGCGAGCGCTGGCCACCAAGTGCACAGCAGCCACACTGAG 773
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 774 GAAGAGCAGTGGCTGTCAGTACGCTGGCCAGGCTGAGGCCATGGCTTTCTTGCAGAG 833
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 834 CAGCCCTTTAGGATTTCTGTACCAAGCCCTTCTACGACAAAGTTTCTGCAGTGGAACTC 893
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
DB 894 TTCGAGATGCAACAGTCTCAGACAGTACTTCACTGAGTTTCAGAGTCTGGGAAAGGT 953
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 954 GGTTTTGGGAGGTATGTGGCTGCAGTGAACCACTGGGAAAGATGTATGCCCTGTAA 1013
QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGluLys 240
DB 1014 AACTGGACAGAGCGGCTGAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAG 1073
QY 241 GluLeuLeuGluLysValSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
DB 1074 GAATCTTTGGAGAGGTTCAGCAGCCCTTTCATTTGCTCTCTGGCCATGCTTTGAGAGC 1133
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
DB 1134 AAGACCCATCTCTGCTTTGTATGAGCCTGTATGAATGGGGGAGACCTCAAGTTCCACATC 1193
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 1194 TACAACGTGGGACGCGTGGCTGGACATGAGCGGGGTATCTTTACTCGGCCAGATA 1253
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 1254 GCCTGTGGAGTGTGCACCTCCATCACTCGGCATCGTCTATCGGACATGAGCCCTGAG 1313
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGCTGGCGGTGAG 1373
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1374 ATGAAGGTGGAGAGCCCATCACCAGAGGCTGGAACCAATGGTTATCGCTCTCTGAG 1433
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1434 ATCTATATGGAAGAGTAAATTTCTCTCTGTGGACTGGTTTGGATGGATGGAGC 1493
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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DB 1494 ATTTATGAAATGGTTGCTGGACGAACACCATTTCAAAGATTCAAAGAAAGTTCAGTAA 1553
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
DB 1554 GAGGATCTGAAGCAAGAACTCTCAAGACGAGGTCAATTTCCAGCATGATAACTTCACA 1613
QY 421 GluLualalaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1614 GAGGAAGCAAAAGATATTTGAGGCTCTTTGCGTAAAGAAACCAGAGCAACGCTTAGGA 1673
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLeuThrIleAsnPhePro 460
DB 1674 AGCAGAGAAAAGTCTGATGATCCCGAGAAAACATCATTTCTTTAAACCATCACTTTCT 1733
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
DB 1734 CGCCTGGAGCTGGCTAAATTTGAACCCCATTTGTGCCAGACCTTCAGTGGTTATGCC 1793
QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspLeuLys 500
DB 1794 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTCCGGGGGTGGAATTTGATGACAAA 1853
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
DB 1854 GATAAGCAGTTCTTCAAAAACCTTTGCGACAGGTGCTGTCTATAGCATGGCAGAGAA 1913
QY 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1914 ATATAGAAACGAGACTGTTTGAGNACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1974 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 2012
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RESULT 5

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US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-738-894A-1
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Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 3 Gaps: 0
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US-10-044-205A-2 (1-553) x US-09-738-894A-1 (1-1662)

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DB 1 ATGTGGACATGGGGGCGCTCGACAACTGATGCCAACACCGCTACTCTCAGCGCCGG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCCTCGGACTCGGACAGCAAGAGCTGAGCGGGCGGTAGCTGGCCCTGGCCC 120
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QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 121 GGGCTGCAGGCTCGCGAGCTCGGCAGAACTGTCCTGAACTTCCACAGAGCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATCGCTCGCGCTCTTCCTCGTCACTTCCTTAGCCACAGTGCCTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
DB 241 CGCAAGCGCGCAACCTTCCTAGAGAGCTGCGAGAACTGGGAGCTGGCGAGAGGACCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAAGACAGCGGCTCGAGGGCTGTGGCCACTTGTGCGAGTGCCTTCCCGCGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCCGCAACCTTCCTCAGCCAGCGCTGCGCCACCAAGTGCCAAAGCAGCCACCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCAGTGGCTGCAGTACGCTGCGCAAGCTGAGGCCATGGCTTTCTTGCAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTAAAGATTTCGTGACCGAGCCCTTCTACGACAGATTCTCGACTGGAACTC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyGly 200
DB 541 TTCGAGATGCAACAGTGTCAAGCAAGTACTTCACTGAGTTTCAGAGTCTGGGAAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 601 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAACACTGGGAAGATGTATGCTGTGAAG 660
QY 221 LysLeuAspLysAlaLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
DB 661 AACTGGHACAGCGCTGAGAGAAAGTGGCGAGAGTGGCTCTCTTGGAAAG 720
QY 241 GluLeuLeuGluLysValSerProPheLeuValSerLeuAlaTyrAlaPheGluSer 260
DB 721 GAAATCTTGGAGAGGTCAAGCCCTTTCATTTCTCTGCGCTATGCTCTTGGAGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 781 AAGACCCATCTCTGCTTGTATGAGCTGTATGAAATGGGGAGACCTCAAGTTCCACATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 841 TACACGTGGGACCGGTGGCTGGACATGAGCCGGTGATCTTTTACTCGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 901 GCCTGTGGATGCTGCACCTCCACTCGCATCGCTATCGGGACATGAAGCCTGAG 960
QY 321 AsnValLeuLeuAspLysLeuCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 961 AATGCTTCTCGAGTACCTCGCAACTGCAGGTATCTGACCTGGGCTGGCGGTGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1021 ATGAAGGTGGCAGCCCATCACCCAGAGGCTGGAACTGTTACATGCTCCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1081 ATCTTAATGGGAAGTAAGTTATTCCTATCTCTGTGGACTGTTTGGCATGGGATGCAGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1141 ATTTATGAATGGTTGCTGGAGCAGACCATTTCAAGATTACAGGAAGAGTTCAGTAAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

DB 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACAGGTCAAATTCAGCATGATACTTCA 1260
QY 421 GluGluAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1261 GAGGAGCAAAAGATATTTTCAGGCTCTTCTTGGCTAAGAAACCCAGAGCAACGCTTAGGA 1320
QY 441 SerArgGluLysSerAspAspProArgLysHisPheLysThrIleAsnPhePro 460
DB 1321 AGCAGAGAAAGTCTGATGATCCAGGAACAATCATTTCTTTAAACGATCACTTTCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProPheValProSerValValTyrAla 480
DB 1381 CGCTGGAAGCTGCGCTAAATTTGAACCCCAATTTGTGCAGACCCCTTCAGTGGTTATGCC 1440
QY 481 LysAspLysAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1441 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTCCGGGGGTGGAAATTTGATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
DB 1501 GATGAAGCAGTTCTTCAAAACTTTGCGACAGGTGCTGTTCTATAGCATGCGAGGAAGA 1560
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTTG 1659
RESULT 6
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1
Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 4 Gaps: 0
US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)
QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
DB 1 ATGGTGGACATGGGGGCCCTCGACAACTGATCGCAACACCGCTACTCGAGGCCCG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCTCGGACTGGACAGCAAGAGCTGCGAGCGCGCGGTAGCTGCGCCCTGCCC 120

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 121 GGGCTGCGAGGGTGGCGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATGGTCGGCGCTCTTCCTGGTACTTCTAGCCACAGTGGCCAGCTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
DB 241 CGCAAGGCGCAACCTTCTAGAGAGCGTGCAGAACTGGGAGCTGGCGAGGAGGACCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAGACAGCGCGCTGAGGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCCCGGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCCGCAACCTTCTAGCCAGGCGGTGGCCACCAAGTGCACAGCAGCCACCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCGAGTGGCTGACGTGCGTGGCCAGGCTGAGGCCATGGCTTCTTTCGAAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTTAAGGATTTCTGACCAAGCGCTTCTACGACAAAGTTCTGCAAGTGGAAATC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
DB 541 TTCGAGATGCAACAGTGTACAGCAAGTACTTCTACTGAGTTCAGAGTGTGGGGAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 601 GGTTTTGGGAGTATGTGCCCTCAGGTGAAACACATGGGGAAGTATGATGCCCTGTAAG 560
QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyLysMetAlaLeuLeuLys 240
DB 661 AAACCTGGACAGAGCGGCTGAAGAAGAAAGGTGGCGAAGATGGCTCTCTTGGAAAG 720
QY 241 GluIleLeuGluLysValSerProPheIleValSerLeuAlaThrAlaPheGluSer 260
DB 721 GAAATCTTGGAGAAGGTACAGAGCCCTTCTCATGTCTCTGGCTATGCCCTTTCAGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 781 AAGACCCATCTGCTTGTATGAGCTGATGATGGGGAGACCTCAAGTTCACATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 841 TACAACGTGGGACGCGTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCACAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 901 GCCTGGGATGCTGCACCTCATGAACCTGGCATCGTCTATCGGACATGAAGCCTGAG 960
QY 321 AsnValLeuLeuAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 961 AATGTCTTCTGGATGACCTCGGCACTGCGAGTTATCTGACCTGGGGCTGGCCCTGGAG 1020
QY 341 MetLysGlyLysPheIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1021 ATGAAGGGTGGCAAGCCCATCCAGAGGGGTGAAACCAATGTTTACATGGCTCCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1081 ATCCCTAAATGGGAAGAGTAAAGTTATTCCTATCTCTGTGGACTGTTTGGCATGGGATGCAGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1141 ATTTATGAATGGTGTGGAGCAACACCATTTCAAGATTAACAGAAAGGTTCAGTAAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

DB 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCATGATAACTTCACA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLysGly 440
DB 1261 GAGGAAGCAAGATATTTGAGGCTCTCTTGGCTAGAAACACAGAGCAGCTTAGGA 1320
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
DB 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
DB 1381 CGCCTGGAGCTGGCTTAATTTGAACCCCATTTGTGCCAGACCTTCAGTGGTTATGCC 1440
QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspLys 500
DB 1441 AAAGACATCGCTGAATTTGATGATTTCTGAGGTTCCGGGGTGGAAATTTGATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
DB 1501 GATAGCAGTCTCTCAAAACCTTTGCGACAGGTGCTTCTTATAGCATGGCAGGAAGA 1560
QY 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGTAATTCATCCAGTCTGGCGTGTTGTTGTTATTG 1659

RESULT 7

US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polym
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3

Alignment Scores:
Pred. No.: 3,7e-206 Length: 1062
Score: 1801.00 Matches: 349
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 62.34% Indels: 0
DB: 3 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-3 (1-1062)

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DB 1 ATGTGGTGCATGGGGCCCTGACAACTGATCGCAACACCGCTTACCTGCGAGCCCGG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCCTCGGACTGGCAGCAAGAGCTGCAGCGCGCGCGGTAGCTTGGCCCTTGCCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60


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Db 121 GGGGTGAGGCGTGGCGGAGACTCGCCAGAGCTGTCCTGAACTTCCACAGCTGTGT 180
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCATCGGTGGCGGCTCTTCGTGACTTCTTAGCCACAGTGCACAGCTTC 240
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
Db 241 CGCAAGCGGCAACCTTCTAGAGACGTGAGAACCTGGAGCTGGCGAGGAGGAGCC 300
Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAGACAGCGCGCTGAGGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCGGG 360
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCCGCAACCTTCTCAGCCAGCGCTGGCCACCAAGTGCACCAAGCAGCAGCAGT 420
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCGAGTGGCTGCAAGTACGCTGGCCAGGCTGAGGCCATGGCTTCTTGCAGAG 480
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTCTGTACCAAGCGCTTCTACGACAAAGTTTCTGCAGTGAAC 540
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyGly 200
Db 541 TTCGAGATGCAACCAAGTGTGACAAAGTACTTCACTGAGTTTCAGAGTCTCGGGAAAG 600
Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 601 GGTTTTGGGAGGTATGTGCGCTCCAGTCAAGTGAACACATGGGAAGATGTATGCTGTAA 660
Qy 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuGluLys 240
Db 661 AAATGGGCAAGAGCGGCTGAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Qy 241 GluLeuGluLysValSerSerProPheIleValSerLeuAlaThrAlaPheGluSer 260
Db 721 GAAATCTTGGAGAGGTGAGAGCGCTTCAATGTCTCTGCGCTATGCTTTCGAGAGC 780
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLysPheHisIle 280
Db 781 AAGACCATCTCTGCTTGTATGAGCTGATGATGGGGAGACCTCAAGTTCCACATC 840
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACGTGGCAGCGCTGGCTGGACATGAGCGCGGTGATCTTTTACTCGGCCAGATA 900
Qy 301 AlaCysGlyMetLeuHisLeuGluGlyIleValTyrArgAspMetLysProGlu 320
Db 901 GCTGTGGATGCTGCACCTCATGAACCTGGCATCGTCTATCGGGACATGAAGCCTGAG 960
Qy 321 AsnValLeuLeuAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Qy 341 MetLysGlyGlyLysProIleThrGlnArg 350
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RESULT 8

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US-10-217-745-3
; Sequence 3, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; Polynucleotides
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; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-3
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Alignment Scores:

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Pred. No.: 3,7e-206 Length: 1062
Score: 1801.00 Matches: 349
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 62.34% Indels: 0
DB: 4 Gaps: 0
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US-10-044-205A-2 (1-553) x US-10-217-745-3 (1-1062)

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Db 1 ATGGTGCACATGGGGGCGCTGGACAACTGATCGCAACACCGCTTACTTCGAGCGCCGG 60
Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 61 AAGCCCTCGGACTCGGACAGCAAGAGCTGCGCGGCGGCGGTAGCTGGCCCTGGCCC 120
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGCAGGCGCTCGCGGAGCTCCGCCAGAAAGCTGCTCCCTGAACTTCCACAGCTGTGT 180
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGCTTC 240
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
Db 241 CGCAAGCGGCAACCTTCTTAGAGACGTGCGAGAACTGGGAGCTGGCCGAGGAGGAGCC 300
Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAGACAGCGCGCTGCGAGGCGTGGTGGCCACTTGTGCGAGTGCCTGCCCGGG 360
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCCGCAACCTTCTCAGCCAGCGCTGGCCACCAAGTGCACCAAGCAGCAGCAGT 420
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCGAGTGGCTGCAAGTACGCTGGCCAGGCTGAGGCCATGGCTTCTTGCAGAG 480
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTCTGTACCAAGCGCTTCTACGACAAAGTTTCTGCAGTGAAC 540
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyGly 200
Db 541 TTCGAGATGCAACCAAGTGTGACAAAGTACTTCACTGAGTTTCAGAGTCTGGGGAAAG 600
Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 601 GGTTTTGGGAGGTATGTGCGCTCCAGTCAAGTGAACACATGGGAAGATGTATGCTGTAA 660
Qy 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuGluLys 240
Db 661 AAATGGGCAAGAGCGGCTGAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Qy 241 GluLeuGluLysValSerSerProPheIleValSerLeuAlaThrAlaPheGluSer 260
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Db 721 GAAATCTTGGAGAGAGTCTAGAGCCCTTTCATTTGTTCTCTGGCCCTATGCGCTTTGAGAGC 780
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAenGlyGlyAspLeuLysPheHisIle 280
Db 781 AAGACCCATCTCTGCTTGTCTATGAGCTGATGAATGGGGAGAGCTTCAAGTTCCACATC 840
Qy 281 TyrAenValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACTGGGCGCGCTGGCTGACATGATGAGCGGGTGATCTTTTACTCGGCCCCAGATA 900
Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db 901 GCCTGTGGGATGCTGCACCTCATGAATCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
Qy 321 AsnValLeuLeuAspAspLeuGlyAenCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db 961 AATGTGCTTCTGGATGACTCGGCNACTGCAAGTTATCTGACCTGGGCTGGCCGTGGAG 1020
Qy 341 MetLysGlyGlyLysProIleThrGlnArg 350
Db 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGG 1050

RESULT 9

US-09-738-894A-3

; Sequence 3, Application US/09738894A

; Patent No. 6331423

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL000636

; CURRENT APPLICATION NUMBER: US/09/738,894A

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 36651

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(36651)

; OTHER INFORMATION: n = A,T,C or G

US-09-738-894A-3

Alignment Scores:

Pred. No.: 8.73e-171 Length: 36651
Score: 1528.00 Matches: 349
Percent Similarity: 41.40% Conservative: 0
Best Local Similarity: 41.40% Mismatches: 1
Query Match: 52.89% Indels: 493
DB: 3 Gaps: 1

US-10-044-205A-2 (1-553) x US-09-738-894A-3 (1-36651)

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Db 2076 ATGTGTGACATGGGGGCCCTGGCAACCTGATGCGCAACACCGGCTACTCGAGCCCGG 2135
Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 2136 AAGCCCTCGACTGGACAGCAAGAGCTGAGCGGGCGCGGTAGCTGGCCCTGCC 2195
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAenPheHisSerLeuCys 60
Db 2196 GGGCTGAGGGCTGCGCGAGCTCGCCAGAGCTGCTCCCTGAACTTCCACAGCCTGTGT 2255
Qy 61 GluGlnGlnProIleGlyArgArgPheArgPheLeuAlaThrValProThrPhe 80
Db 2256 GAGCAGAGCCCATCGGTGCGCGGCTCTTCGTGACTTCTTAGCCACAGTGCACCGTTC 2315

Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAenThrGluLeuAlaGluGluGlyPro 100
Db 2316 CGCAAGCGCGCAACCTTCTTAGAGACGTCGAGAACCTGGAGCTGGCCGAGAGGAGCC 2375
Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 2376 ACCAAGACAGCGGCTGACGGGCTGGTGCCACTTGTGGAGTGGCCCTGCCCCGGGG 2435
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 2436 AACCCGCAACCTTCTTCCAGCCAGCGCTGCCACCAAGTCCCAAGCAGCCACCACTGAG 2495
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 2496 GAAGAGCAGTGGCTGACGTGACGTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 2555
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnThrLysLeu 180
Db 2556 CAGCCCTTTAAGGATTTCTGTACCAGCGCCCTTACGACAAAGTTTCTGCAGTGGAAACTC 2615
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db 2616 TTCGAGATGCAACCACTGTCAGACAGTACTTCTCAGATTTCAGAGTCTGGGGAAGGT 2675
Qy 201 GlyPheGlyGlu----- 204
Db 2676 GGTTTTGGGAGGTAAGTGTCTCCAGTAGCCAGGCTAGAAAGTGAAGCATAGAGCATGA 2735
Qy 204 ----- 204
Db 2736 AAGGGGTAAATGTTGGCCTTTCTTTTAAATCTCAGTTACTTAGAACTAATTTTCAGCAC 2795
Qy 204 ----- 204
Db 2796 CATATGTGGAGATTCTAGCCCCGTCTCCCCAGCCCCCTTCTTTGTGTGTGCCATGTG 2855
Qy 204 ----- 204
Db 2856 TGAATAAAACACAAATGGCATGAGAGAGACAAAGCAAAATTTATACTTGGCCAGACTCT 2915
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Db 2916 GTCATGGGTCTTCATTAGGAACGTGTGAGATGCTGGACACTTCAGAGAATGATAGCAA 2975
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Db 2976 TGTGTGACAGAGATCTCCGTTTCCCTTAATTTGTGATAATGAAGGCACCTTCAGAAAAA 3035
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Db 3036 TGGATATTTAAGAAAAATACTCTAACTAGCTGGGTGTGTGACACTGCCTGTATCCAGCT 3095
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Qy 204 ----- 204


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Db 2436 AACCCGCAACCCCTTCTCTAGCCAGCGCGTGGCCACCAAGTGCACAGCCACCACTGAG 2495
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Db 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db 2556 CAGCCCTTTAAGGATTCGTGACCAAGCGCTTCTACGACAAAGTTCCTGCAGTGGAAACTC 2615
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Db 201 GlyPheGlyGlu- 204
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Db 2676 GGTTTTGGGAGGTAAAGTGTCTCCAGTAGCCAGGCTAGAGGTGAAGCATAGAGCATGA 2735
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Db 2736 AAGGGGTAAATGTTGCTTCTTTTAAATCTCAGTTACTTAGAACTAATTTCCAGCAC 2795
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Db 204 - 204
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Db 2796 CATATGTGGAGGATTTCTAGCCCGCTCTCCAGCCCGCTTCTTTGTGTGTGCCATGGTG 2855
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Db 2856 TGAATAAAACNCAATGGCATGAGAGAGACNAGCAAAATTTATACTTGGCCNAGACTCT 2915
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Db 204 - 204
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Db 2916 GTCATGGGTCTCCATTAGGAACGTGCTGAGATGCCTGGACACTTCAGAGAAATGATAGCAA 2975
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Db 204 - 204
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Db 3216 AAGAAAGAAAGAAAGAAAGAAACACTTATCTTGAAGTAAGGTTGAGAACCTGTTTTGT 3275
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Db 204 - 204
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Db 3276 ACCACTGTTGTGCCAGCTTCTCTGTTTTTAAGTAATAAAAAATATTTTCAGGTAAATTTG 3335
QY |||||
Db 204 - 204
QY |||||
Db 3336 CTTGATATAAACTAACCAATTAACCTGTTTTAAATGTACATGCAGTGGCACTTCGCACA 3395
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Db 204 - 204
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Db 3396 AATGCAATGTTGGTGAAGCAACACTCAATCTGGATCCAAAGACACTCTCATCACCCCTGT 3455
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Db 204 - 204
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Db 3456 GCCCATTAAATAGTGCTCCCATCCCTCTCTCTCCAGCCCTGACACCACTAGTCCGC 3515
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Db 204 - 204
QY |||||
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Db 3516 TTTCTGTCTCTAGGGAATTTGCCTATTCTGGGGTGTTCACAAATATGTGACCCCTTTGTGT 3575
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Db 3576 CTGGCTTCTTTCACCTCAATTAGAAATGTTTTTGGGGTTCATTACACCTGTAGCATGTCAA 3635
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Db 204 - 204
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Db 3636 TACTCCATTCCTTTTATGGCTGTATAATATTTCCATCGTATGGATGTACTACATTTTCATG 3695
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Db 204 - 204
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Db 3696 TAGCCATTCACTCTGTTGATGGACACTTGGGCTGTTTTTCCCTTTTGGCTATTGTGTATGG 3755
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Db 204 - 204
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Db 3756 TGCTGCTATTATGCACAAAGTATTGTTTGAATCCTTGTGTTTCATTCTCTTTGGATTAT 3815
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Db 204 - 204
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Db 3816 GCCCAGGAGTGAATTTCTAGGGCATATGGTGATACTATGTTTAACTTTTCAAGGAGCCA 3875
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Db 204 - 204
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Db 3876 CAAAACCTTTCACATTTTTTATTTCCACCACGAATGCTTAAAGGTTTCGATTTCTCCACA 3935
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Db 204 - 204
QY |||||
Db 3936 TCCTTGCCCAACACTTGATATTTTCTGTATTTTTTTTATGAAGGCTGCTAGTAGGTGA 3995
QY |||||
Db 204 - 204
QY |||||
Db 3996 AGGAGTATGCACCTGTAGTCCCACTTTTCTTGAGAACACTTCTTATTTTACAGCTACTC 4055
QY |||||
Db 204 - 204
QY |||||
Db 4056 CTTTCTCCAATGCTTAACATCTTTTCCACCCACCTCTCTCTTATCATCTCCACCTCTCTG 4115
QY |||||
Db 205 - 208
QY |||||
Db 4116 CAGTACCATCTACTTCTTACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4175
QY |||||
Db 208 lGlnValLysAsnThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLys 228
QY |||||
Db 4176 CCAGGTGAAATAAACAACCTGGGAAGATGATGCTGTAAAGAAACTGGACAAGACGGCTGAA 4235
QY |||||
Db 228 sLysLysGlyGlyGlyLysMetAlaLeuLeuGluLysGluLysLeuLysValSerSe 248
QY |||||
Db 4236 GAAGAAAGGTGGCAGAGATGGCTCTCTTGGAAAAGGAAATCTTTGGAGAAGGTGAGCAG 4295
QY |||||
Db 248 rPropheileValSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMe 268
QY |||||
Db 4296 CTTTTCATTTCTCTCTGGCTATGCTTTGAGGCAAGACCCATCTCTGCTTGTCTAT 4355
QY |||||
Db 268 tSerLeuMetAsnGlyAspLeuLysPheHisLeuTyrAsnValGlyThrArgGlyLe 288
QY |||||
Db 4356 GAGCTGTATGAATGGGGAGACCTCAAGTTCACATCTACAACGTGGGCGCGCTGCT 4415
QY |||||
Db 288 uAspMetSerArgValLlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHi 308
QY |||||
Db 4416 GGACATGAGCGGGTGATCTTTTATCTCGGCCAGATAGCTGTGGGATGCTGCACCTCCA 4475
QY |||||
Db 308 sGluLeuGlyLysValTyrArgAspMetLysProGluAsnValLeuLeuAspLeuG1 328
QY |||||
Db 4476 TGAATCTGGCATCTGTCTATCGGACATGAGCCTGAGAAATGTGCTTCTGGATGACCTGG 4535
QY |||||
Db 328 yAsnCysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyLysProIleTh 348
QY |||||
Db 4536 CAATGCAAGTTATCTGACCTGGGCTGGCGTGGAGATGAAGGTGGCAAGCCCATCAC 4595
QY |||||
Db 348 rGlnArg 350
QY |||||
Db 4596 CCAGAGG 4602
QY |||||
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RESULT 11

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US-09-614-748A-7
; Sequence 7, Application US/09614748A
; Patent No. 6660474
; GENERAL INFORMATION:
; APPLICANT: FELDER, ROBIN A.
; APPLICANT: JOSE, PEDRO
; TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
; FILE REFERENCE: FELDER 3.9-001 CONT
; CURRENT APPLICATION NUMBER: US/09/614,748A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: PCT/US99/00663
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/071,199
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/098,279
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-748A-7

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US-09-417-197-60
; Sequence 60, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 60
; LENGTH: 2511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: G-rk5-EGFP fusion
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2508)
US-09-417-197-60

Alignment Scores:
Pred. No.: 1.27e-139 Length: 2511
Score: 1252.50 Matches: 259
Percent Similarity: 63.07% Conservative: 103
Best Local Similarity: 45.12% Mismatches: 162
Query Match: 43.33% Indels: 50
DB: 4 Gaps: 11

US-10-044-205A-2 (1-553) x US-09-417-197-60 (1-2511)

Qy 7 LeuAspAenLeuLeuAlaAenThrAlaTyrluGlnAlaArgLysProSerAspCysAsp 26
Db 7 CTGGAACATCGTGGCCCAACACGCTCTTGCTGAAAGCCAGGAGGGGGGAGGAAAG 66

Qy 27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
Db 67 CGCAAGGGGAAAGCAAGAGTGGAAAGAAATCCTGGAAGTTCCCTCACATTAGCCAGTGT 126

Qy 46 AlaGluLeuArgGlnLysLeuSerLeuAenPheHisSerLeuGlnGlnGlnProle 65
Db 127 GAAGACCTCCGAAGGACCATGACAGAGATTACTGACGTTTATGTGCAAGCAGCACAATC 186

Qy 66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
Db 187 GGGAGGCTGCTTTTCCGGCAGTTTGTGAAACCAAGGCTGGGCTGGAGTGTACATTGAG 246

Qy 86 PheLeuGluAspValGlnAenTrpGlu-----LeuAlaGluGluGly 99
Db 247 TTCTCGGACTCGTGGCAGAAATATGAAGTTACTCCAGATGAAAACTGGGAGAGAAAGG 306

Qy 100 ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
Db 307 -----AAGGAAATTATGACCAAGTACCTC-----ACCCCA 336

Qy 120 GlyAenPro-----GlnProPheLeuSerGlnAlaValAlaThr 132
Db 337 AAGTCCCTGTTTTCATAGCCCAAGTGGCCCAAGACCTGGTCTCCAGCAGGAGAGAG 396

Qy 133 LysCysGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeuArgLysAla 152
Db 397 CTCCTACAGAGCGGTGCAAGAACTCTTCTGCTGCTGTCACAGCTCTGTCCACGAG--- 453

Qy 153 GluAlaMetAlaPheLeuGlnGlnProPheLysAspPheValThrSerAlaPheTyr 172
Db 454 -----TACCTCAGGAGGAGAACCAATCCACGAATATCTGGACAGCATGTTTTTT 501

Qy 173 AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
Db 502 GACCGCTTTTCCAGTGGAGGTGGTGGAAAGGCAACCGGTGACCAAAAAACACTTTTCAGG 561
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Qy 193 GluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAen 212
Db 562 CAGTATCGAGTGTAGGAAAGGGGGCTTCGGGGAGGTCTGTGCTGCGCAGGTTCGGGCC 621

Qy 213 ThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysGlyGly 232
Db 622 ACGGTAATAATGTATGCTCGAAGCGCTTGAGAAAGAGAGATCAAAAAGGAAAGG 681

Qy 233 GluLysMetAlaLeuLeuGluLysGluLeuGluLysValSerSerProPheIleVal 252
Db 682 GAGTCCATGGCCCTCAATGAGAAGCAGATCTCCGAGAAGGTCAACAGTCAGTTTGTGTC 741

Qy 253 SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAen 272
Db 742 AACCTGGCTATGCTTACGAGCAAGGATGACCTGTGCTTGGTCTCTGACCATCATGAT 801

Qy 273 GlyGlyAspLeuLysPheHisIleTyrAenValGlyThrArgGlyLeuAspMetSerArg 292
Db 802 GGGGTGACCTGAAGTTCCATCTACAACTAGGCAACCCCTGGCTTCCGAGGAGGCGG 861

Qy 293 ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIle 312
Db 862 GCCTGTTTATGCGGAGAGATCTCTGCGCTTAGAAGACCTCCACCGTGAGAACC 921

Qy 313 ValTyrArgAspMetLysProGluAenValLeuLeuAspLeuGlyAenCysArgLeu 332
Db 922 GTCTACCGAGATCTGAAACCTGAAACATCTCTGTATGATGATTATGGCCACATTAGGATC 981

Qy 333 SerAspLeuGlyLeuAlaValGluMetLysGlyLysProIleThrGlnArgAlaGly 352
Db 982 TCAGACCTGGGCTTGGCTGTGAAGTCCCGAGGAGACCTGATCCGCGCGGGTGGGC 1041

Qy 353 ThrAenGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal 372
Db 1042 ACTGTTGGCTACATGGCCCCCGAAGTCTCTGAACACAG---AGTAGCGCTGAGCCCC 1098

Qy 373 AspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLys 392
Db 1099 GACTACTGGGCGCTTGGCTGCTCATCTATGAGATGATCGAGGGCCAGTCGCGCTTCGCG 1158

Qy 393 AspTyrLysGluLysValSerLysGluAspLysGlnArgThrLeuGlnAspGluVal 412
Db 1159 GGCGTAAAGGAGAGGTGAAGCGGAGGAGGTGAGCCCGGGTCTCGAGACGAGGAG 1218

Qy 413 LysPheGlnHisAspAenPheThrGluAlaLysAspIleCysArgLeuPheLeuAla 432
Db 1219 GTGTACTCCAC---AAGTTCTCCAGAGAGCCCAAGTCCATCTGCAAGATGCTGCTCAG 1275

Qy 433 LysLysProGluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHis 451
Db 1276 AAAGATGCGAAGCAGAGGCTGGGCTGCGAGGAGGAGGGGCTGCGAGAGTCAAGAGACAC 1335

Qy 452 HisPhePheLysThrIleAenPheProArgLeuGluAlaGlyLeuIleGluProPhe 471
Db 1336 CCCTTCTTCAGGAACATGAACCTCAAGCGCTTAGAAGCGGGATGTTTCGACCCCTCCCTTC 1395

Qy 472 ValProAspProSerValTyrAlaLysAspIleAlaGluIleAspAspSerGlu 491
Db 1396 GTTCAGACCCCGCGCTGTGTACTGTAAAGACGTGTGGACATCGACAGTCTTCCACT 1455

Qy 492 ValArgGlyValGluPheAspLysAspLysGlnPhePheLysAenPheAlaThrGly 511
Db 1456 GTGAAGGCGTCAATCTGGACCACACAGACGACGACTTCTACTCCAAGTCTCCACGGGC 1515

Qy 512 AlaValProIleAlaTrpGlnGluIleIleGluThrGlyLeuPheGluGluLeuAen 531
Db 1516 TCTGTGTCCATCCCATGCGCAACAGATGATAGAAACAGAAATGCTTTAAGGAGCTGAAC 1575

Qy 532 -----AspPro-AsnAr 535
Db 1576 GTGTTTGACCTAATGTGTACCTCCCGCCAGATCTGAACAGAAACACCCCTCCGGAACCG 1635

Qy 535 gpro---ThrGlyCysGluGluGlyAenSerSerLysSer 547
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Db 1636 CCCAAGAAAGGCTGCTCCAGAGACTCTTCAAGCGGCAGC 1675
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RESULT 13

US-09-417-197-42

; Sequence 42, Application US/09417197

; Patent No. 6518021

; GENERAL INFORMATION:

; APPLICANT: Ole THASTRUP, et al.

; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An

; FILE OF INVENTION: On A Cellular Response

; FILE REFERENCE: 3759-0110P

; CURRENT APPLICATION NUMBER: US/09/417,197

; CURRENT FILING DATE: 1999-10-07

; NUMBER OF SEQ ID NOS: 143

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 42

; LENGTH: 2529

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: EGFP-Grk5 fusion

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2526)

US-09-417-197-42

Alignment Scores:

Pred. No.:	1,29e-139	Length:	2529
Score:	1252.50	Matches:	259
Percent Similarity:	63.07%	Conservative:	103
Best Local Similarity:	45.12%	Mismatches:	162
Query Match:	43.35%	Indels:	50
DB:	4	Gaps:	11

US-10-044-205A-2 (1-553) x US-09-417-197-42 (1-2529)

QY 7 LeuAspAsnLeuAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
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Db 763 CTGAAACATCGTGCCCAACACGCTCTGCTGAAAGCAGGAGGAGGCGGAGAAAG 822
QY 27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
||||| :|||
Db 823 CGCAAGGGGAAAGCAAGAAAGTGAAGAAATCTCCATGATCCCTCAGATAGCCAGTGT 882
QY 46 AlaGluLeuArgGlnLysSerLeuAsnPheHisSerLeuCysGluGlnProIle 65
||||| :|||
Db 883 GAAGACCTCCGAGGACCATGACAGAGATTTACTGAGTTTATGTGCAAGCAGCCAAATC 942
QY 66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
||||| :|||
Db 943 GGGAGGCTGCTTTTCCGGCAGTTTGTGAAACCCAGGCTGGGCTGGAGTGTACATTCCAG 1002
QY 86 PheLeuGluAspValGlnAsnTrpGlu-----LeuAlaGluGluGly 99
||||| :|||
Db 1003 TTCCTGGACTCGCTGGCAGATATGAAAGTTACTCCAGATGAAATACTGGGAGAAAGGG 1062
QY 100 ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
||||| :|||
Db 1063 -----AGGAAATATGACCAAGTACCTC-----ACCCCA 1092
QY 120 GlyAsnPro-----GlnProPheLeuSerGlnAlaValAlaThr 132
||||| :|||
Db 1093 AAGTCCCTGTTTTCATAGCCCAAGTTGGCCAAAGACCTGGTCTCCACAGCGAGGAGAAG 1152
QY 133 LysCysGlnAlaAlaThrThrGluGluArgValAlaAlaValThrLeuArgLysAla 152
||||| :|||
Db 1153 CTCCTACCAAGCGCTGCAAGAACTCTTTTCTGCTGTGCACATCTGTCACAG--- 1209
QY 153 GluAlaMetAlaPheLeuGlnGlnProPheLysAspPheValThrSerAlaPheTyr 172
||||| :|||
Db 1210 -----TACCTGAGGGGAGAACCATTTCCAGAAATATCTGGACAGCATGTTTTTT 1257

QY 173 AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
||||| :|||
Db 1258 GACCGCTTTCTCCAGTGGAGTGGTTGAAAGGACCGGTGACCAAAAAACACTTTCAGG 1317
QY 193 GluPheArgValLeuGlyLysGlyPheGlyGluValCysAlaValGlnValLysAsn 212
||||| :|||
Db 1318 CAGTATCGAGTGTAGGAAAGGGGCTTCCGGAGAGGTCTGTGCTGCCAGGTTCGGGCC 1377
QY 213 ThrGlyLysMetTyrAlaCysGlyLysLeuAspLysLysArgLeuLysLysGlyGly 232
||||| :|||
Db 1378 ACGGTAAATATGATGCTGCAAGCGCTTGAGAGAGAGAGATCAAAAGAGGAAAGG 1437
QY 233 GluLysMetAlaLeuGluLysGlnIleLeuGluLysValSerSerProPheIleVal 252
||||| :|||
Db 1438 GAGTCCATGGCCCTCAATGAGAGCAGATCTCCAGAAAGGTCAACAGTCAGTTGTGTC 1497
QY 253 SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
||||| :|||
Db 1498 AACCTGGCTATGCTACGAGACCAAGGATGCACTGTGCTTGGTCTCTGACCATCATGAAT 1557
QY 273 GlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArg 292
||||| :|||
Db 1558 GGGGTGACCTGAAAGTTCCACATCTACAACATGGGCAACCCCTGGCTTCGAGGAGGAGCGG 1617
QY 293 ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuGluLeuGlyIle 312
||||| :|||
Db 1618 GCCTTGTATTATGGCGCAGAGATCTCTGCGGCTTAGAGACCTCCACCGTGAGAACACC 1677
QY 313 ValTyrArgAspMetLysProGluAsnValLeuLeuAspLeuGlyAsnCysArgLeu 332
||||| :|||
Db 1678 GTCTACCGAGATCTGAAACCTGAAACATCTGTTAGATGATTATGGCCACATTAGGATC 1737
QY 333 SerAspLeuGlyLeuAlaValGluMetLysGlyLysProIleThrGlnArgAlaGly 352
||||| :|||
Db 1738 TCAGACCTGGGCTTGGCTGTGAAGATCCCGAGGAGACCTGATCCGCGCGCGGTGGGC 1797
QY 353 ThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal 372
||||| :|||
Db 1798 ACTGTTGGCTACATGGCCCCCGGAAGTCTTGAAACACAG---AGGTACGGCTCAGCCCC 1854
QY 373 AspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLys 392
||||| :|||
Db 1855 GACTACTGGGCGCTTGGCTGCTCATCTATGAGATGATCGAGGGCCAGTCCGCTCCGC 1914
QY 393 AspTyrLysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluVal 412
||||| :|||
Db 1915 GCGCGTAAGGAGAAAGGTGAAGCGGGAGGAGGTGGACCGCGGGTCTGGAGACGGAGAG 1974
QY 413 LysPheGlnHisAspAsnPheThrGluAlaLysAspIleCysArgLeuPheLeuAla 432
||||| :|||
Db 1975 GTGTACTCCAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCAGC 2031
QY 433 LysLysProGluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHis 451
||||| :|||
Db 2032 AAAGATCGAAGCAGAGAGCTGGGCTGCGAGGAGGGGGGTGCAGAGGTCAAGAGACAC 2091
QY 452 HisPhePheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProPhe 471
||||| :|||
Db 2092 CCCTTCTTCCAGAACATGAATCTCAAGCGCTTAGAGCGGGAGTGGACCTCCCTTC 2151
QY 472 ValProAspProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGlu 491
||||| :|||
Db 2152 GTTCCAGACCCCGCGCTGTGTACTGTGAAGGACGTGTGTGACATCGAGAGTCTTCCACT 2211
QY 492 ValArgGlyValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGly 511
||||| :|||
Db 2212 GTGAAGGGCGTCAATCTGGACCAACAGACGACACTTCTACTCCAAAGTTCTCCACGGGC 2271
QY 512 AlaValProIleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
||||| :|||
Db 2272 TCTGTGTCATCCATCCGCAAAAGAGATGATAGAAACAGATGCTTTTAGGAGCTGAAC 2331
QY 532 -----AspPro-AsnAr 535

Db 2332 GTGTTGGACCTAATGGTACCTCCGCCGAGATCTGAACAGAAACACCCCTCCGAGACCG 2391
Qy 535 gPro---ThrGlyCysGluGluGlyAAsnSerSerLyssSer 547
Db 2392 CCCAAGAAAGGGCTGCTCCAGAGACTCTTCAAGCGCGCAGC 2431

RESULT 14

US-09-016-434-1298
; Sequence 1298, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1298:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2557 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G306804
US-09-016-434-1298

Alignment Scores:
Pred. No.: 1,31e-139 Length: 2557
Score: 1252.50 Matches: 259
Percent Similarity: 63.07% Conservative: 103
Best Local Similarity: 45.12% Mismatches: 162
Query Match: 43.95% Indels: 50
DB: 4 Gaps: 11

US-10-044-205A-2 (1-553) x US-09-016-434-1298 (1-2557)

Qy 7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
Db 227 CTGGAACACATCGTGCCCAACACGCTTCTGCTGAAAGCCAGGAAGGGGGCGGAGGAAAG 286
Qy 27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
Db 287 CGCAAGAGGAAAGCAAGAGTGGAAAGAAATCCTTGAAGTTCCCTCACCATTAGCCAGGTGT 346

Qy 46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnPheProIle 55
Db 347 GAAGACCTCCCAAGAGGACCATAGACAGATTCAGTCTTTATGTGCAAGCAGGCAATTC 406
Qy 66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
Db 407 GGGAGGCTGCTTTCCGGCAGTTTTGTGAACACGAGCCTGGGCTGGAGTGTTCATCTCAG 466
Qy 86 PheLeuGluAspValGlnAsnTrpGlu-----LeuAlaGluGly 99
Db 467 TTCTCTGAGTCCGTGGCAGAAATATGAAGTTACTCCAGATGAAAAACTGGGAGAAAGGG 526
Qy 100 ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
Db 527 -----AAGGAAATATGACCAAGTACCTC-----ACCCCA 556
Qy 120 GlyAsnPro-----GlnProPheLeuSerGlnAlaValAlaThr 132
Db 557 AAGTCCCTCTGTTTCATAGCCCAAGCTGGTCTCCAGACGAGGAGGAAG 616
Qy 133 LysCysGlnAlaAlaThrThrGluGluArgValAlaAlaValThrLeuArgLysAla 152
Db 617 CTCCTACAGAAAGCGTGCAGAAAGAACTCTTTCTGCTGTGCACAGCTGTCTCCACGAG--- 673
Qy 153 GluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyr 172
Db 674 -----TACCTGAGGGGAGAACCATTTCCAGCAATATCTGGACAGCATGTTTTT 721
Qy 173 AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
Db 722 GACCGCTTCTCCAGTGGAGTGGTTGGAAGGCAACCGGTGACCAAAACACTTTTCAGG 781
Qy 193 GluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsn 212
Db 782 CAGTATCGAGTGTAGGAAGAGGGGCTTCGGGAGGTCCTGCTGCCAGTTCGGGCC 841
Qy 213 ThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysGlyGly 232
Db 842 ACGGGTAAATGTATGCTGCAAGCGCTTGGAGAGAGAGAGATCAAAAGAGGAAGGG 901
Qy 233 GluLysMetAlaLeuGluLysGluIleLeuGluLysValSerSerProPheIleVal 252
Db 902 GAGTCCATGGCCCTCAATGAGAGCAGATCTCTGAGAAGGTCACACAGTCAGTTGTGTC 961
Qy 253 SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
Db 962 AACCTGGCTATGCTACGACACCAAGATGCACCTGCTGCTGGTCTCTGACCATCATGAT 1021
Qy 273 GlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArg 292
Db 1022 GGGGGTGACCTGAAGTTCACATCTACAACATGGGCAACCCCTGGCTTCGAGGAGGAGCGG 1081
Qy 293 ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIle 312
Db 1082 GCCTTGTGTTTATGGCGCAGAGATCCTCTGCGGCTTTAGAAAGACCTCCACCGTGAGAACACC 1141
Qy 313 ValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeu 332
Db 1142 GTCTACCGAGATCTGAAACCTGAAACATCTCTGTAGATGATTATGGCCACATTAGGATC 1201
Qy 333 SerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGly 352
Db 1202 TCAGACCTGGGCTTGGCTGTGAAGTCCCGAGGAGACCTGATCCGCGCGCGGGTGGGC 1261
Qy 353 ThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal 372
Db 1262 ACTGTGTGCTACATGGCCCCGAAATCTCTGAACACCAACAG---AGGTACGGCTTGAGCCCC 1318
Qy 373 AspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLys 392
Db 1319 GACTACTGGGGCCCTTGGCTGCTCTATCATGAGATGATCGAGGGGCTCCCGCTTCCGC 1378
Qy 393 AspTyrLysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluVal 412

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OM protein - nucleic search, using frame_plus_p2n model
Run on: May 11, 2005, 04:38:46 ; Search time 766 Seconds
(without alignments)
4418.383 Million cell updates/sec

Title: US-10-044-205A-2
Perfect score: 2889
Sequence: 1 MVDGALDNLNTAYLQAR.....NRPTGCEBGNSSKGVCLLL 553

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5662332 seqs, 3060109652 residues
Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_NA -QFM=fastap -SUFFIX=rnpb -MINMATCH=0.1
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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10044205 @CNC 1.1 723 @runat_09052005_180053_28978
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2889	100.0	1659	13	US-10-044-205A-3	Sequence 3, Appli
2	2889	100.0	2198	13	US-10-044-205A-1	Sequence 1, Appli
3	2883	99.8	1662	9	US-09-802-117-1	Sequence 1, Appli
4	2883	99.8	1662	14	US-10-217-745-1	Sequence 1, Appli
5	2883	99.8	1662	17	US-10-311-034-45	Sequence 45, Appl
6	2883	99.8	1662	17	US-10-451-168-49	Sequence 49, Appl
7	2883	99.8	1662	9	US-10-788-197-22	Sequence 22, Appl
8	2883	99.8	2249	9	US-09-802-117-5	Sequence 5, Appli
9	2883	99.8	2249	14	US-10-217-745-5	Sequence 5, Appli
10	2876	99.6	1662	9	US-09-964-469-1	Sequence 1, Appli
11	2876	99.6	1662	16	US-10-425-962-1	Sequence 1, Appli
12	2823.5	97.7	1701	17	US-10-072-012-273	Sequence 273, App
13	1801	62.3	1062	9	US-09-802-117-3	Sequence 3, Appli
14	1801	62.3	1062	14	US-10-217-745-3	Sequence 3, Appli
15	1528	52.9	36651	9	US-09-964-469-3	Sequence 3, Appli
16	1528	52.9	36651	16	US-10-425-962-3	Sequence 3, Appli
17	1283.5	44.4	1737	16	US-10-325-430-2	Sequence 2, Appli
18	1283.5	44.4	1737	19	US-10-788-197-18	Sequence 18, Appl
19	1283.5	44.4	2113	16	US-10-325-430-1	Sequence 1, Appli
20	1280.5	44.3	2113	19	US-10-677-983-7	Sequence 7, Appli
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22	1258	43.5	1683	19	US-10-788-197-6	Sequence 6, Appli
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24	1252.5	43.4	1773	19	US-10-788-197-12	Sequence 12, Appl
25	1252.5	43.4	2467	15	US-10-084-817-110	Sequence 110, App
26	1252.5	43.4	2511	14	US-10-072-036-60	Sequence 60, Appl
27	1252.5	43.4	2519	13	US-10-071-766-13	Sequence 13, Appl
28	1252.5	43.4	2529	14	US-10-072-036-42	Sequence 42, Appl
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30	1252.5	43.4	2557	17	US-10-305-720-1298	Sequence 1298, Ap
31	1252.5	43.4	2557	17	US-10-380-235-7	Sequence 7, Appli
32	1252.5	43.4	2557	18	US-10-775-169-77	Sequence 77, Appl
33	1252.5	43.4	2557	18	US-10-723-860-2591	Sequence 2591, Ap
34	1250.5	43.3	1599	19	US-10-788-197-20	Sequence 20, Appl
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36	1245.5	43.1	2519	10	US-09-971-392-72	Sequence 72, Appl
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38	1243.5	43.0	2017	19	US-10-677-983-8	Sequence 8, Appli
39	1239	42.9	1738	19	US-10-788-197-10	Sequence 10, Appl
40	1239	42.9	2848	10	US-09-873-367C-142	Sequence 142, App
41	1239	42.9	2848	17	US-10-159-856-4	Sequence 4, Appli
42	1239	42.9	2848	19	US-10-843-641A-142	Sequence 142, App
43	1235.5	42.8	2558	18	US-10-723-860-6729	Sequence 6729, Ap
44	1235	42.7	2817	17	US-10-388-334-621	Sequence 621, Appl
45	1233	42.7	2848	9	US-09-851-686-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-044-205A-3
; Sequence 3, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-3

Alignment Scores:

Pred. No.: 0 Length: 1659
Score: 2889.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-044-205A-3 (1-1659)

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DB 61 AAGCCTCGGACTGGCAGCAGAAAGCTGCAGCGCGCGCGCTAGCCTGCCCCCTGCC 120
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DB 121 GGGCTGCAGGCTGGCGGAGCTCGCCAGAGCTGTCCCTGAACCTTCCACAGCCCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATCGCTCGCGCCCTCTTCGTGACTTCCAGCCACAGTGCCTCCAGTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTyrGluLeuAlaGluGlyPro 100
DB 241 CCACAGCGCGCAACCTTCTAGAGAGCTGCAGAACTGGAGCTGGCGAGGAGGAGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCAGTGGCTGCAGTACGCTGCAGAGGCTGAGGCCATCGCTTCTTGCAGAG 480
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QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuLys 240
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QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 781 AAGACCCATCTCTGCTTGTATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC 840
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QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
DB 1501 GATAAGCAGTTCTTCAAAAACCTTTGCGACAGTGTCTGTCTATAGCATGCGAGGAAGA 1560
QY 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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RESULT 2

US-10-044-205A-1

; Sequence 1, Application US/10044205A

; Publication No. US2002012346A1

; GENERAL INFORMATION:

; APPLICANT: KAPPELLER-LIBERMANN, Rosana

; APPLICANT: BANDARU, Rajasekhara

; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein

; TITLE OF INVENTION: Uses Thereof

; FILE REFERENCE: 10147-52U1

; CURRENT APPLICATION NUMBER: US/10/044, 205A

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: US 60/242,428

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: US 60/241,884

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: US 60/241,877

; PRIOR FILING DATE: 2000-10-20

; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 2198
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-044-205A-1

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 Score: 2889.00 Matches: 553
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US-10-044-205A-2 (1-553) x US-10-044-205A-1 (1-2198)

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 Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 471 GAGCAGCAGCCCATCGGTGGCGGCTCTTCGTGACTTCCAGCCACAGTGCACAGTTC 530
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 Db 711 GAAGAGCGAGTGGCTGCAGTACGCTGGCAGAGCTGAGGCCATGGCTTCTTTCGCAAGAG 770
 Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 771 CAGCCCTTTAGGATTTCTGACAGCGCTCTACGACACAGTTTCTGCAGTGGAACTC 830
 Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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 Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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 Qy 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGlyLys 240
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 Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
 Db 1071 AAGACCCATCTCGCCTTGTATGAGCCTGATGAATGGGGAGAGCCTCAAGTTCACATC 1130

Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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 Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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 Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 Db 1251 AATGTGCTTCTGGATGACCTCGCAACTGCAAGTTATCTGACCTGGGCTGGCCGTGGAG 1310
 Qy 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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 Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1371 ATCTTAATGGAAAGGTAAAGTTATTCCTATCTGTGGACTGGTTTGGCCATGGGATGCAGC 1430
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 Db 1671 CGCTCGAAGCTGGCTTAATTTGAACCCCAATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1730
 Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspLys 500
 Db 1731 AAAGACATCGCTGAAATTTGATGATTTCTCAGGTTTCGGGGGGTGGAAATTTGATGACAAA 1790
 Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 Db 1791 GATAGCAGTTCTTCAAAAACCTTTGCGACAGGTGCTGTCTCTATAGCATGGCAGGAGNA 1850
 Qy 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1851 ATTATAGAAACGGGACTGTTTGGAGNACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
 Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1911 GAGGGTATTCATCAAGTCTGGCGTGTGTTGTTATTG 1949

RESULT 3

US-09-802-117-1
 ; Sequence 1, Application US/09802117
 ; Publication No. US20020042503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polym
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT APPLICATION NUMBER: US/09/802,117
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 60/188,449
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-802-117-1

Alignment Scores:

Pred. No.: 0 Length: 1662
 Score: 2883.00 Matches: 552
 Percent Similarity: 99.82% Conservativity: 0
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 9 Gaps: 0

US-10-044-205a-2 (1-553) x US-09-802-117-1 (1-1662)

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 Db 121 GGGCTGCAGGGCTGGCGGAGCTCGCCAGAACGTCTCCTGNACTTTCACAGCCCTGTGT 180
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 Db 301 ACCAAGACAGCGCGCTGCAGGGCTGGTGGCACTTGTGGAGTGCCTTGCCTGCCCGGG 360
 Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 361 AACCGCAACCTTCTCAGCCAGCGCGTGGCCACCAAGTGCACAGCAGCCACTGAG 420
 Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 421 GAAGAGCGAGTGGCTGCAGTACGCTGGCCAGGCTGAGGCCATGGCTTCTTGCAGAG 480
 Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 481 CAGCCCTTTAGGATTTGTGACAGCGCTTCTACGACAGATTTCTGCGAGTGGAACTC 540
 Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 541 TTCGAGATGCAACCAAGTGTGACACAAGTACTTCACTGAGTTTCAGAGTGTGGGAAAGGT 600
 Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAAAACACTGGGAAGATGTATGCTGCTGAAG 660
 Qy 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuGluLys 240
 Db 661 AAACCTGGACAGACGGCTGAGAAAGAGGTGGCGAGAGATGGCTCTCTTGGAAAG 720
 Qy 241 GluLeuLeuGlyLysValSerSerProPheLeuValSerLeuAlaTyrAlaPheGluSer 260
 Db 721 GAAATCTTGGAGAGGTGAGAGCCCTTCACTGTCTCTGGCCCTATGCTGCTTGGAGGC 780
 Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisLe 280
 Db 781 AAGACCCATCTCTGCTTGTATGAGCTGTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 841 TACAACGTGGGACGCGTGGCTGGACATGAGCCGGGTGATCTTTTACTTCGCCCCAGATA 900
 Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 Db 901 GCCTGTGGATGCTGCACCTCATGAACTCGGCATCGTCTATCGGACATGAAGCCTGAG 960
 Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 Db 961 AATGTGCTTCTGGATGACCTCGCAACTGCAAGGTATATCGACCTGGGCTGGCCGTGAG 1020
 Qy 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1021 ATGAAGGTGGCAAGCCCATCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
 Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1081 ATCCTAATGAAAAAGGTAAGTTATTCCTATCCTGTGACTGGTTTGCCTATGGATGCAGC 1140
 Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1141 ATTTATGAAATGGTGTCTGGACGAACACCATTCAAAGATTACAAGGAAAAAGTCAGTAAA 1200
 Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 Db 1201 GAGATCTGAAGCAAGAGACTCTGACAGCAGGTCAATTCACAGCATGATTAATTTCACA 1260
 Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACACAGACCAACGCTTAGGA 1320
 Qy 441 SerArgGluLysSerAspAspProArgLysHisPheLysThrIleAsnPhePro 460
 Db 1321 AGCAGAAAAAGTCTGATGATCCAGGAAAAATCATTTCTTTAAACCATCAACTTTCTCT 1380
 Qy 461 ArgLeuGluAlaGlyLeuLeuGluProPheValProAspProSerValValTyrAla 480
 Db 1381 CGCTCGAGAGCTGGCTTAATTTGAACCCCATTTGTGCCAGACCTTTCAGTGGTTATGCC 1440
 Qy 481 LysAspIleAlaGluLeuAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
 Db 1441 AAAGACATCGCTGAAATTTGATTTCTCTGAGGTTCGGGGGGTGGAAATTTGATGACAAA 1500
 Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
 Db 1501 GATAAGCAGTTCTTTCAAAACCTTTTGCAGCAGGTCTGTCTCTATAGCATGGCAGGAAGA 1560
 Qy 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1561 ATTATAGAACGGGACTGTTTGAAGAACTGAATGACCCCAACACACCTACGGTTGTGAG 1620
 Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 4

US-10-217-745-1
 ; Sequence 1, Application US/10217745
 ; Publication No. US20030004328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilkanowski, Nathaniel L.
 ; APPLICANT: Walker, D. Wade
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
 ; TITLE OF INVENTION: Polynucleotides
 ; TITLE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT APPLICATION NUMBER: US/10/217,745
 ; CURRENT FILING DATE: 2002-08-12
 ; PRIOR APPLICATION NUMBER: US/09/802,117
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1662

TYPE: DNA

ORGANISM: homo sapiens

US-10-217-745-1

Alignment Scores:

Alignment Scores:				
Pred. NO.:	0	Length:	1662	
Score:	2893.00	Matches:	552	
Percent Similarity:	99.8%	Conservative:	0	
Best Local Similarity:	99.8%	Mismatches:	1	
Query Match:	99.79%	Indels:	0	
DB:	14	Gaps:	0	

US-10-044-205A-2 (1-553) X US-10-217-745-1 (1-1662)

Qy	1	MetValAspMetGlyAlaLeuAspAsnLeuLeuAlaAenThrAlaIaTyLeuGlnAlaArg	20
Db	1	ATGGTGGACATGGGGGCCCTGGAYAACTGATCGCCAACACCGCTACTCTGCAGAGCCGG	60
Qy	21	LysProSerAspCysAspSerLysGluLeuGlnArgArgAGTgSgSerLeuAlaLeuPro	40
Db	61	AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGCGGTAGCCTGGCCCTGGCCC	120
Qy	41	GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAenPheHisSerLeuCys	60
Db	121	GGGCTGCAGGGCTGCGCGGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCGCTGTGT	180
Qy	61	GluGlnGlnProIleGlyArgArgLeuPheArgaspPheLeuAlaThrValProThrPhe	80
Db	181	GAGCAGCAGCCCATCGGTGCGCGCCTCTTCGGTGACTTCTTAGCCACAGTGCACAGTTC	240
Qy	81	ArgLysAlaAlaThrPheLeuGluAspValGlnAenTrpGluLeuAlaGluGluGlyPro	100
Db	241	CGCAAGCCGGCAACCTTCTAGAGAGCGTGCAGAACTGGGAGCTGGCGGAGGAGGAGCC	300
Qy	101	ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	120
Db	301	ACCAAGACAGCGCGCTGCAGGGCTGCTGGCCACTTGTGCGAGTGGCCCTGCCCCGGGG	360
Qy	121	AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu	140
Db	361	AACCCGCAACCTTCTCAGCCAGCGCCGTGGCCACCAGTGCCAAGCAGCGCCACCATGAG	420
Qy	141	GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu	160
Db	421	GAAGACCGAGTGGCTGCAGTGACCTGGCCAAAGCTGAGGCCATGGCTTTCTTGCAAGAG	480
Qy	161	GlnProPheLysAspPheValThrSerAlaPheTyrrAspLysPheLeuGlnTrpLysLeu	180
Db	481	CAGCCCTTTTAAAGGATTTCTGTACCAAGCGCCCTTCTACGACAAGTTTCTGCAGTGGAACTC	540
Qy	181	PheGluMetGlnProValSerAspLysTyrrPheThrGluPheArgValLeuGlyLysGly	200
Db	541	TTGCGAGATCCAAACAGGTGTACAGCAAGTACTTCACTGAGTTACAGAGTGTGGGGAANGGT	600
Qy	201	GlyPheGlyGluValCysAlaValGlnValLysAenThrGlyLysMetTyrrAlaCysLys	220
Db	601	GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAAGATGATGCTGTAAAG	660
Qy	221	LysLeuAspLysIleArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGluLys	240
Db	661	AAACTGGAACAAGCGCGCTGAAGAAGAAGAGGTGGCGAGAAAGATGGCTCTCTTGGAAAAG	720
Qy	241	GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrrAlaPheGluSer	260
Db	721	GAATCTTGGAGNAGGTGAGCAGGCCCTTTCATTGTCTCTCTGGCCCTATGCTTTTGAGAC	780
Qy	261	LysThrHisLeuCysLeuValMetSerLeuMetAenGlyGlyAspLeuLysPheHisIle	280
Db	781	AAGACCCTACTCTGCTTGTGATGAGCTGTGAATGGGGAGACCTCAAGTTTCCACATC	840

Qy	281	TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle	300
Db	841	TACAACGTGGGCACGCCTGGCTGGACATGAGCGCGGTGATCTTTTACTCGGCCACGATA	900
Qy	301	AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu	320
Db	901	GCCTGTGGGATGCTGCACCTCCATGAACCTCGGCATGCTCTATCGGACATGAAGCCTGAG	960
Qy	321	AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu	340
Db	961	AATGTGCTCTGGATGACCTCGGCAACTGCGAGGTTATCTGACCTGGCGCTGGCGCTGGAG	1020
Qy	341	MetIysGlyGlyIysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu	360
Db	1021	ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACTCAATGGTTATCATGGCTCTCGAG	1080
Qy	361	IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer	380
Db	1081	ATCCTAATGGANAAGGTAAAGTTATTCCTATCTCTGTGGACTGGTTGGCCATGGGATGCAGC	1140
Qy	381	IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys	400
Db	1141	ATTTATGAAATGGTGTCTGGACGAACACCACTTCAAAGATTACAAAGGAAAAAGGTCAGTAAA	1200
Qy	401	GluAspLeuLysGlnArgThrLeuGlnAspGluValIysPheGlnHisAspAsnPheThr	420
Db	1201	GAGGATCTGAAGCAAGAAGACTCTGCAAGACGAGGTCAATTTCCAGCATGATAAATCTTCACA	1260
Qy	421	GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly	440
Db	1261	GAGGAACAAAGATATTTCGAGGCTCTTCTTGCTTAAGAAAAACGAGCAACGCTTAGGA	1320
Qy	441	SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro	460
Db	1321	AGCAGAGAAAAGTCTGATGATCCCGAGAAACATCATTTCTTTAAACGATCAACTTTCTCT	1380
Qy	461	ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla	480
Db	1381	CGCCTGGNAGCTGGCTTAATTGAACCCCAATTTGTGCCAGACCCCTTCAGTGGTTTATGCC	1440
Qy	481	LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys	500
Db	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTCCGGGGGTGGAAATTTGATGACAAA	1500
Qy	501	AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu	520
Db	1501	GATAAGCAGTCTTTCAAAAACTTTTGGACAGGTGCTGTCTTCATTAGCATCGCAGGAGAA	1560
Qy	521	IleIleGluThrGlyLeuPheGluLeuLysAsnAspProAsnArgProThrGlyCysGlu	540
Db	1561	ATTATAGAAACGGGACTGTTTGGAGAACTGAAATGACCCCAACAGACCTACGGGTGTGAG	1620
Qy	541	GluGlyAsnSerLysSerGlyValCysLeuLeuLeu	553
Db	1621	GAGGGTAATTCACCAAGTCTGGCGTGTGTTTGTATTG	1659

RESULT 5

US-10-311-034-45

US-10-311-034-43
: Sequence 45, Application US/10311034

; sequence 43, Application 93/103
; Publication No. US20040023242A1

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: YUE, Henry

APPLICANT: LAL, Preeti

APPLICANT: BANDMAN, Olga

APPLICANT: BOROWSKY, Mark L.

APPLICANT: AU-YOUNG, Janice

APPLICANT: LU, Yan

APPLICANT: GANDHI, Ameena R.

APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: CHAWLA, Narinder K.

APPLICANT: YAO, Monique G.

; APPLICANT: LU, Dyung Aina M.

APPLICANT: GREENWALD, Sara R.
 APPLICANT: RAMKUMAR, Jayalaxmi
 APPLICANT: GRIFFIN, Jennifer A.
 APPLICANT: KEARNEY, Liam
 APPLICANT: BURFORD, Neil
 APPLICANT: NGUYEN, Damiel B.
 APPLICANT: TANG, Y. Tom
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: HE, Ann
 APPLICANT: THORNTON, Michael
 APPLICANT: HAFALIA, April
 APPLICANT: ARVIZU, Chandra S.
 APPLICANT: GURURAJAN, Rajagopal
 APPLICANT: LO, Terence P.
 APPLICANT: KHAH, Farrah A.
 APPLICANT: RECIPON, Shirley A.
 APPLICANT: AZIMZAI, Yalda
 APPLICANT: POLICKY, Jennifer L.
 APPLICANT: DING, Li
 APPLICANT: GREYHER, Megan
 APPLICANT: ELLIOTT, Vicki S.
 APPLICANT: THANGAVELU, Kavitha
 APPLICANT: BATRA, Sajeev
 APPLICANT: ISON, Craig H.
 TITLE OF INVENTION: HUMAN KINASES
 FILE REFERENCE: PI-0125 PCT
 CURRENT APPLICATION NUMBER: US/10/311,034
 CURRENT FILING DATE: 2002-12-10
 PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
 60/228,056
 PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
 NUMBER OF SEQ ID NOS: 52
 SOFTWARE: PERL Program
 SEQ ID NO 45
 LENGTH: 1662
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
 US-10-311-034-45

Alignment Scores:
 Pred. No.: 0 Length: 1662
 Score: 2883.00 Matches: 552
 Percent Similarity: 99.82% Conservative: 0
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 17 Gaps: 0
 US-10-044-205A-2 (1-553) x US-10-311-034-45 (1-1662)

Qy	1	MetValAspMetGlyAlaLeuAspSerLeuLeuAlaAsnThrAlaTyrLeuGlnAlaArg	20
Db	1	ATGGTGGACATGGGGGCGCTGGACAACTGATCGCAACACCGCTACCTGCGAGCGCGG	60
Qy	21	LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro	40
Db	61	AAGCCTCGACTGGACAGCAAGAGCTGCGAGCGCGGCGGTAGCTGGCCCTGCC	120
Qy	41	GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys	60
Db	121	GGGCTGCGAGGCTGCGCGAGCTCGCCAGAAAGCTGCTCCGAACTTCCACAGCCTGTGT	180
Qy	61	GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe	80
Db	181	GAGCAGCAGCCCATCGGTGCGCGCTCTTCGTGACTTCCTAGCCACAGTGCACAGTTC	240
Qy	81	ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro	100
Db	241	CGCAAGCGGCGCACTTCTTAGAGGAGCTGTCAGAACTGGAGCTGGCGAGGAGGCC	300

Qy	101	ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	120
Db	301	ACCAAGACACGCGCTGCGAGGGCTGTCGCCACTTGTGCGAGTGCCTTGCCTGCGGGG	360
Qy	121	AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu	140
Db	361	AACCGCAACCTTCTTCAGCCAGCGCTGCGCCACCAAGTCCCAAGCAGCCACCACTGAG	420
Qy	141	GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu	160
Db	421	GAAGAGCAGTGGCTGCGAGTGCAGCTGCCAAGGCTGAGCCATGGCTTCTTTCGACAG	480
Qy	161	GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu	180
Db	481	CAGCCCTTAAAGGATTCGTGACCCAGCGCTTTCAGACAAAGTTTCTCAGTGGAAATC	540
Qy	181	PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly	200
Db	541	TTGAGATGCAACCAAGTGTACACAAGTACTTCACTGAGTTTCAGAGTCTCGGGAAAGGT	600
Qy	201	GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys	220
Db	601	GGTTTGGGAGGTATGTGCGCTCAGGTGAANAACACTGGGAAGATGATGCTCTGAAG	660
Qy	221	LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys	240
Db	661	AACTGGCAAGAAGCGCTCAAGAAGAAGGTGGCAGAAAGATGGCTCTCTTGGAAAG	720
Qy	241	GluLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer	260
Db	721	GAATCTTTGGAGAAGGTGAGCAGCCCTTTCATTTCTCTCTGGCTTATGCTCTTGGAGC	780
Qy	261	LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle	280
Db	781	AAGACCAATCTCTGCTTGTCTGATGAGCTGATGAGTGGGGAGACCTCAAGTTCCACATC	840
Qy	281	TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle	300
Db	841	TACAACGTGGGCACGCGCTGACATGACATGCGGGGTGATCTTTTACTCGGCCAGATA	900
Qy	301	AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu	320
Db	901	GCCTGTGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG	960
Qy	321	AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu	340
Db	961	AATGTGCTTCTGGATGACCTCGCAACTGCGAGGTATCTGACCTGGGGCTGGCGTGGAG	1020
Qy	341	MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu	360
Db	1021	ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAAACCAATGGTTACATGGCTCCTGAG	1080
Qy	361	IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer	380
Db	1081	ATCTTAATGGAAGAGTAAGTTATTCCTATCTCTGTGAGCTGGTTTGGCATGGATGACG	1140
Qy	381	IleTyrGluMetValAlaGlyValThrProPheLysAspTyrLysGluLysValSerLys	400
Db	1141	ATTTATGAATGGTGTGTGGACGACCACTTCAAGATTACAGAGAAAGGTGAGTAA	1200
Qy	401	GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr	420
Db	1201	GAGGATCTGAAGCAAGAACTCTCAAGACGAGGTCAAAATCCAGCATGATAACTTACA	1260
Qy	421	GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly	440
Db	1261	GAGGAAGCAAAAGATATTTGAGGCTCTTCTTGGCTAAGAAACAGAGCAACGCTTAGGA	1320
Qy	441	SerArgGluLysSerAspProArgLysHisPhePheLysThrIleAsnPhePro	460
Db	1321	AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTCT	1380
Qy	461	ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValTyrAla	480

Db 1381 CCGCTGGAGCTGGGCTTAATTAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1440
Qy 481 LysAspIleAlaGluLeuAspPheSerGluValArgGlyValGluPheAspPheLys 500
Db 1441 AAAGACATCGCTGAATTCCTCTGAGGTCGGGGGTGGAATTTGATGACAAA 1500
Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGlu 520
Db 1501 GATAGCAGTTCCTCAAAACCTTTCGACAGGTCGTGTTCTTATAGCATGGCAGGAGAA 1560
Qy 521 IleIleGluThrGlyLeuPheGluLeuLeuAsnProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGAGGAACCTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGTAATTCATCCAGTCTGGCGTGTGTTGTTATG 1659

RESULT 6

US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-49

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 17 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-451-168-49 (1-1662)

Qy 1 MetValAspMetGlyValLeuAspPheLeuIleAlaAsnThrAlaThrLeuGlnAlaArg 20
Db 1 ATGGTGGACATCGGGGCCCTTGACAACTGATCGCCACACCGCTACCTGCGAGGCCGG 60
Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgSerLeuAlaLeuPro 40

Db 61 AAGCCCTCGACTCGGACAGCAAGAGCTGCAGCGGCGCGGCTAGCCTGGCCCTGCCC 120
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGCAGGCTCGCGGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCCTGTGT 180
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCATCGGTCGCCCTCTTCCTGCTGACTTCCTAGCCACAGTGGCCACGTTT 240
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
Db 241 CGCAAGCGCGCAACTTCTTAGAGAGCTGCAGAACTGGGAGCTGGCGAGGAGGAGCC 300
Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAAGACAGCGCGCTGCAGGGCTGGTGCCACTTGTGCGAGTGCCTGCCCCGGGG 360
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCCGCAACCTTCTCAGCAGCGCGTGCCCAAGTAGTCCCAAGCAGCCACCACTGAG 420
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCAGTGGCTGCGAGTGACGTCGCCAAGGCTGAGGCCATGGCTTTCTTGCACAG 480
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyArgLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTCTGTCAGCCAGCGCTTCTACGACAAAGTTTCTCAGTGGAACTC 540
Qy 181 PheGluMetGlnProValSerAspLysTyThrThrGluPheArgValLeuGlyLysGly 200
Db 541 TTCGAGATGCAACCAAGTGTCAACAAGTACTTCACTGAGTTTCAGAGTCTCTGGGAAAGGT 600
Qy 201 GlyPheGlyGluValCysAlaValGlnValLysValThrGlyLysMetTyAlaCysLys 220
Db 601 GGTTTTGGGAGGTATGTGCCGTCCAGGTGAAAACACTGGGAAGATGATGCTCTGTAG 660
Qy 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuLys 240
Db 661 AAACCTGGACAGAGCGGCTGACAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG 720
Qy 241 GluLeuLeuGluLysValSerSerProPheIleValSerLeuAlaTyAlaPheGluSer 260
Db 721 GAAATCTTTGGAGAGGTGAGCAGCGCTTTCATTGTCTCTCTGGCCTATGCTCTGAGAGC 780
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
Db 781 AAGACCCCATCTCTGCCCTTGTATGAGCCCTGATGAATGGGGAGAGCTCAAGTTCCACATC 840
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTySerAlaGlnIle 300
Db 841 TACAACGTGGGACGCGTGCGCTGGACATGAGCGGGTGATCTTTTACTCGGCCCAGATA 900
Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyArgAspMetLysProGlu 320
Db 901 GCCTGTGGATGCTGCACCTCCATGAACTCGCATCGTCTATCGGGACATGAAGGCTCAG 960
Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuLeuAlaValGlu 340
Db 961 AATGTGCTTCCTGGATGACCTCGGCAACTGCGAGGTATCTGACCTGGGGCTGGCCGTGGAG 1020
Qy 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyTrpMetAlaProGlu 360
Db 1021 ATGAAGGTGGCAAGCCCATCACCAGAGGGCTGGAAACCAATGGTTACATGGCTCTCAG 1080
Qy 361 IleLeuMetGluLysValSerTySerTyProValAspTrpPheAlaMetGlyCysSer 380
Db 1081 ATCTAATGGAAGTAAGTTATTCCTATCTCTGTGGACTGTTTGTCCATGGGATGCAGC 1140
Qy 381 IleTyGluMetValAlaGlyArgThrProPheLysAspTyLysGluLysValSerLys 400
Db 1141 ATTTATGAAATGGTGTGGAGCAACACCATTTCAAAGATTACAAGGAAAGGTTCAGTAAA 1200

QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
DB 1201 GAGGATCTGACGACCAAGAACTCTGACAGCAGAGGTCAATTTCCAGCATGATACTTCACA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1261 GAGGAAGCAAAAGATATTGTCAGGCTCTTTGGCTAAGAAACACAGAGCAACGCTTAGGA 1320
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
DB 1321 AGCAGAGAAAGCTGATGATCCAGGAAACATCATTTCTTTAAACCATCAACTTTCTCT 1380
QY 461 ArgLeuGluAlaGluLeuIleGluProPheValProAspProSerValValIleAla 480
DB 1381 CGCTGGAAAGCTGGCTTAATGAACCCCATTTGTGCCAGACCTTCAGTGGTTATGCC 1440
QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTCGGGGGTGGAATTTGATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGlu 520
DB 1501 GATAAGCAGTCTCTCAAAACATTTTCGACAGGTGCTGTCTTATAGCATGCGAGGAAGA 1560
QY 521 IleIleGluThrGlyLeuPheGluLeuLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATTATAGAAACGGGACTGTTGAGGAACTGATGACCCCAACAGACCTACGGTGTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 7

US-10-788-197-22
; Sequence 22, Application US/10788197
; Publication No. US20050032125A1
; GENERAL INFORMATION:
; APPLICANT: OAKLEY, ROBERT H.
; APPLICANT: HUDSON, CHRISTINE C.
; TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
; FILE REFERENCE: NRK.108
; CURRENT APPLICATION NUMBER: US/10/788,197
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/14581
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,986
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/401,698
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-197-22

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 19 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-788-197-22 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
DB 1 ATGGTGGACATGGGGGGCCCTGACAACTGATCGCAACACCGCTACTCGAGGCCCGG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgSerLeuAlaLeuPro 40

DB 61 AAGCCCTCGGACTCGGACAGCAAGAGCTGCAGCGGGCGGCTAGCCTGGCCCTGCCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 121 GGGCTGACGGGCTCGGGGAGCTCCGCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATCGTGGCGGCTCTTCGTGACTTCCTAGCCACAGTCAGTGCACCGTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
DB 241 CGCAAGCGCGCAACCTTCTTAGAGACGTGCAGAACTGGGAGCTGGCGAGGAGGAGGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAAGACACGGCGCTGCAGGGGCTGTGGCCACTTGTGGAGTGGCCCTGCCCCGGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCCGCAACCCCTTCTCAGCCAGCGCGTGGCCACCAAGTGCACAGCAGCCACCATGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCAGTGGCTGAGTGCAGTGCAGCTGCCAAGCTGAGGCCATGGCTTTCTTCAAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTTAAGGATTTTCGTGACCAAGCCCTTTCACGACCAAGTTCTGCAGTGGAAACTC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
DB 541 TTCAGATGCAACCCAGTGTGACACAAGTACTTCACTGAGTTCAGAGTGTCTGGGGAAGGT 600
QY 201 GlyPheGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 601 GGTTCGGGAGGTATGTGCGCTCAGTGAAGAACTGCGAAGATGTATGCTCTGTAAG 660
QY 221 LysLeuAspLysArgLeuLysLysGlyGlyLysMetAlaLeuLeuGluLys 240
DB 661 AAATCGACAAAGAGCGGCTGAAGAAAGGTGGCAGAAAGATGGCTCTCTTGGAAAG 720
QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
DB 721 GAATCTTGGAGAAGGTGACAGCCCTTTCATCTCTCTGGCTATGCTCTTTGAGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 781 AAGACCCATCTCTGCTTGTGATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 841 TACAACGTGGGACGCGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 901 GCCTGTGGATGCTGCACCTCCATGAACTGGCATCGTCTATCGGGACATGAAGCCGTGAG 960
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCGTGGAG 1020
QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGCTGGAACCAATGTTATCATGGCTCCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1081 ATCTATATGNAAGGTAGTATTCTTCTGACTGCTGACTGTTTGGCATGGGATGACAGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400

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Db 1141 ATTTATGAATGGTTGCTGGACCAACACCATTCATAAGATTACAGAAAAAGTCTAGTAAA 1200
Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
Db 1201 GAGGATCTGAAGCAAAAGAACTCTGCAAGACGAGGTCATAATTCCAGCATGATAACTTTCACA 1260
Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
Db 1261 GAGGAAGCAAAAGATATTGTCAGGCTCTCTTGGCTAAAGAAACCCAGAGCAACGCTTAGGA 1320
Qy 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAACATCAATTTCTTTAAACCATCAACTTTCTCT 1380
Qy 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
Db 1381 CGCTTGAAGCTGGCTTAATTGAACCCCATTTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1440
Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db 1441 AAAGACATCGCTGAAATTTGATGATTTCTGAGGTTTCGGGGGTGGAATTTGATGACAAA 1500
Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGluGlu 520
Db 1501 GATAGCAGTGTCTTCAAAACTTTTCGACAGGTGCTGTCTCTATAGCATGGCAGGAAGAA 1560
Qy 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGAGGAACCTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGTAAATCATCAAGTCTGGCGTGTGTTGTTATTG 1659

RESULT 8
US-09-802-117-5
; Sequence 5, Application US/09802117
; Publication No. US20020042503A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444561 Human G-Coupled Protein Receptor Kinases and Polym
; FILE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Alignment Scores:
Pred. No.: 0 Length: 2249
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 9 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-5 (1-2249)
Qy 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 354 ATGTGGACATGGGGGCTTGGACAACTGATCGCAACACCGCTACTCGACGCGCGG 413
Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
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Db 414 AAGCCCTCGGACTGGACAGCAAGAGCTGCAGCGCGCGGCTAGCTGGCCCTGCCCC 473
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysSerLeuAsnPheHisSerLeuCys 60
Db 474 GGGCTGCAGGGCTGCGGGAGCTCCGCCAGAAAGCTGTCCCTGNACTTCCACAGCCCTGTGT 533
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 534 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCTGCTGACTTCTAGCCACAGTGGCCACGTTTC 593
Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
Db 594 CGCAGGCGGCAACCTTCTTAGAGACGTGCAGAACTGGAGCTGGCCAGGAGGAGGCC 653
Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 654 ACCAAAGACAGCGCTGCAGGGCTGGTGCCACTTGTGCGAGTGGCCCTGCCCCCGGG 713
Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 714 AACCCGCAACCTTCTTCAGCCAGCGCGTGGCCCAACAAAGTGCACAGCAGCCACTGAG 773
Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 774 GAAGAGCGAGTGGCTGCACTGACCTGCCAAGGCTGAGGCCATGGCTTTCTTTCAGAG 833
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 834 CAGCCCTTTAAGGATTTGTCGACCCAGCGCTTCTACGACAAAGTTTCTGCAGTGGAACTC 893
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db 894 TTCGAGATGCACCAAGTGTGCAGCAAGTACTTCACTGAGTTTCAGAGTCTCGGGGAAAGT 953
Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 954 GGTTTTGGGGAGGTATGTGCGCTCAGGTGAAAACACTGGGAAAGATGTATGCCCTGTAG 1013
Qy 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGlyLys 240
Db 1014 AAACCTGGACAGAGCGGCTGAGAGAAAGAGTGGCAGAGAGATGGCTCTCTTGGAAAG 1073
Qy 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db 1074 GAAATCTTGGAGAAAGTTCAGCAGCCCTTTCATTTGTCTCTCTGGCTATGCTCTTTCAGAGC 1133
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
Db 1134 AAGACCCATCTCTGCTTGTTCATGAGCCTGATGAATGGGGAGAGCTCAAGTTCCACATC 1193
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 1194 TACAACGTGGGCACGCGTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 1253
Qy 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db 1254 GCCTGTGGATGTCTCCACTCCATGAACTCGCATCGTCTATCGGGACATGAAGCTCGAG 1313
Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuLeuAlaValGlu 340
Db 1314 AATGTGCTTCTGGATGACCTCGCAACTGCAAGGTATCTGACCTGGGGCTGGCCCTGGAG 1373
Qy 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db 1374 ATGAAGGTGGCAAGCCCATCCAGAGGGCTGGACCAATGGTTACATGGCTCTGAG 1433
Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
Db 1434 ATCTAATGAAAAAGGTAAGTTATTCCTATCTGTGGACTGGTTTGGCCATGGGATGCAGC 1493
Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
Db 1494 ATTTATGAATGGTTGCTGGAGCAACCACTTCAAGAGATTACAAGGAAAAAGGTTCAGTAAA 1553
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QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
DB 1554 GAGGATCTGAGCAAGAAAGAACTCTGCAGACAGAGGTCAAAATTCACGATGATAACTTTCACA 1613
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1614 GAGGAAGCAAAAGATATTTCGAGGCTCTCTTGGCTAAGAAACACAGACCAACGCTTAGGA 1673
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
DB 1674 AGCAGAGAAAGTCTGATGATCCCAAGAAACATCATTTCTTTAAACGATCAACTTTTCT 1733
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValThrAla 480
DB 1734 CGCTGGAGAGTGGCTTAATGAACCCCATTTGTCAGACACCTTCAGTGGTTATGCC 1793
QY 481 LysAspIleAlaGluLysAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1794 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTGCGGGGTGGAATTTGATGACAAA 1853
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGlu 520
DB 1854 GATAAGCAGTTCTTCAAAACATTTTCGACAGCTGCTGTTCTATAGCATGCGAGGAAGA 1913
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1914 ATTATAGAAACGGGACTGTTTGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1974 GAGGTAATTCATCCAACTCTGGCGTGTGTTGTTATTG 2012

RESULT 9
US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Milgowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases an
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-5

Alignment Scores:
Pred. No.: 0 Length: 2249
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 14 Gaps: 0

US-10-044-205A-2 (1-553) x US-10-217-745-5 (1-2249)
QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaThrLeuGlnAlaArg 20
DB 354 ATGGTGGACATGGGGGCCCTGGACACCTGATCGCAACACCGCTACTCTGACGGCCGG 413
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
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DB 414 AAGCCCTCGGACTCGCAGCAAGAGCTGCAGCGCGCGCGCTAGCCTGGCCCTGCGCC 473
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 474 GGGCTGAGGGCTCGCGGGAGCTCCGCAGAAAGCTGCTCCCTGAACTTCCACAGCCTGTGT 533
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 534 GAGCAGCAGCCCATCGCTCGCGGCTCTTCGTGACTTCTTAGCCACAGTGCACCGTTC 593
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
DB 594 CGCAAGCGCGCAACTCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCGAGGAGGAGCC 653
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 654 ACCAAAGACACGCGCTGCAGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCCCCGGGG 713
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 714 AACCCGCAACCTTCTCAGCCAGCGCTGGCCACCAAGTGCACAGCAGCCACCACTGAG 773
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 774 GAAGAGCAGTGGCTGAGTGACGTGACCTGCCAAGCTGAGGCTATGGCTTTCTTGCACAG 833
QY 161 GlnProPheLysAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
DB 834 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTACGACCAAGTTCCTGACGTGGAACCTC 893
QY 181 PheGluMetGlnProValSerAspLysThrPheThrGluPheArgValLeuGlyLysGly 200
DB 894 TTCGAGATGCAACCAAGTGTGACACAGTACTTCTACTGAGTTCAGAGTCTGGGGAAGGT 953
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 954 GGTGTTGGGGAGGTATGTGCGCTCAGGTGAAAAACACTGGGAAAGATGTATGCTCTGAAG 1013
QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuLys 240
DB 1014 AAATGACAGAAAGCGCTGAAAGAAAGGTGGGAGAAAGATGGCTCTCTTGGAAAG 1073
QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaThrAlaPheGluSer 260
DB 1074 GARATCTTGGAGAGGTGACAGCCCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGAGAGC 1133
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
DB 1134 AAGACCATCTCTGCTTGTGATGAGCTGATGATGAGGAGGAGACCTCAAGTTCACATC 1193
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 1194 TACAACGTGGGACGCGTGGCTGGACATGAGCGGGGTGATCTTTTACTCGGCCAGATA 1253
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
DB 1254 GCCTGTGGATGCTGCACCTCCATGAACTCGGCATGCTATCTCGGACATGAAGCCTGAG 1313
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGGTATCTGACCTGGGGCTGGCGCTGGAG 1373
QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1374 ATGAAGGTGGCAAGCCCATCACCAGAGGCTGGAAACCAATGTTACATGGCTCTCTGAG 1433
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1434 ATCTTAATGAAAGGTAAAGTTATCTCTGCTGAGCTGTTTGGCATGGATGCGAGC 1493
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1494 ATTTATGAAATGGTGTGCTGGACGAACCACTTCAAGAGTTTACAAGGAAAGAGTTCAGTAA 1553
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QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAenPheThr 420
|||
DB 1554 GAGGATCTGAGCAAGAAAGAACTCTGCAAGACGAGGTCAAATTCAGCATGATAACTTCACA 1613
|||
QY 421 GluGluAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
|||
DB 1614 GAGGAAGCAAAAGATATTTCAGGGCTCTTCCTGGCTAAGAAACCAAGAGCAACGCTTAGGA 1673
|||
QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAenPhePro 460
|||
DB 1674 AGCAGAAAGTCTGATGATCCAGGAAACATCATCTTTTAAACGATCACTTTCT 1733
|||
QY 461 ArgLeuGluAlaGlyLeuLysGluProPheValProAspProSerValValTyrAla 480
|||
DB 1734 CGCTTGGAGCTGGCTTAATTAACCCCAATTTGTGCCAGACCTTCAGTGGTTTATGCC 1793
|||
QY 481 LysAspIleAlaGluLysAspPheSerGluValArgGlyValGluPheAspPheLys 500
|||
DB 1794 AAAGACATCGCTGAATGATATTCTCTGAGGTTCGGGGGTGGAATTTGATGACAAA 1853
|||
QY 501 AspLysGlnPhePheLysAenPheAlaThrGlyAlaValProIleAlaTyrGlnGlu 520
|||
DB 1854 GATAGCAGTCTTCAAAACTTTCGACAGGTGCTGCTTATAGCATGGCAGGAGAA 1913
|||
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAenAspProAenArgProThrGlyCysGlu 540
|||
DB 1914 ATTATAGAAACGGGACTGTTTCAGGAACCTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973
|||
QY 541 GluGlyAenSerSerLysSerGlyValCysLeuLeuLeu 553
|||
DB 1974 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG 2012
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RESULT 10
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1
Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 9 Gaps: 0
US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)
QY 1 MetValAspMetGlyValAlaLeuAspAenLeuIleAlaAenThrAlaTyrLeuGlnAlaArg 20
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DB 1 ATGGTGGACATGGGGCCCTGACAACTGATCGCAACACCGCTACCTACCTGCGAGCCCGG 60
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QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
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DB 61 AAGCCCTCGGACTGGCAGCAGCAAGAGCTGCAGCGCGCGCGCTAGCTGGCCCTGCCCC 120
QY GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAenPheHisSerLeuCys 60
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DB 121 GGGCTGCAAGGCTGCGCGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
|||
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
|||
DB 181 GAGCAGCAGCCATCGGTGCGCGCTTCCGTGACTTCTTAGCCACAGTGCCTCCAGTTC 240
|||
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAenTyrGluLeuAlaGluGlyPro 100
|||
DB 241 CGCAAGCGCGCAACCTTCTAGAGACCTGCAGAACTGGAGCTGGCCGAGGAGGACCC 300
|||
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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DB 301 ACCAAAGACAGCGCTGCGAGGGCTGTGGCCACTTGTGGAGTGGCCCTGCCCGGGG 360
|||
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaThrThrGlu 140
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DB 361 AACCGCAACCTTCTCAGCCAGCGCTGGCCACCAAGTGCACAGCAGCCACCTAG 420
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QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGln 160
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DB 421 GAAGAGCAGGTGGCTGCGAGTGCAGCTGGCCAGGCTGAGGCTGGCTTCTTTCGAAG 480
|||
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
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DB 541 TTCGAGATGCAACCAAGTGTGACAAAGTACTTCTACGAGTTCAGAGTTCGCGGGAAGGT 600
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QY 201 GlyPheGlyGluValCysAlaValGlnValLysAenThrGlyLysMetTyrAlaCysLys 220
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DB 601 GGTITTTGGGAGGTATGTGCCGTGAGGTGAAACACTGGGAAAGTATGATGCCCTGTAAG 660
|||
QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGlyLys 240
|||
DB 661 AAATCGACAGAGAGCGCTGAGAGAAAGGTGGCGAGAGATGCTCTCTTGGAAAG 720
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QY 241 GluLeuLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
|||
DB 721 GAAATCTTGGAGAAAGTTCAGCAGCGCTTCTTCTCTCTGCGCTATGCTCTGAGAGC 780
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QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAenGlyGlyAspLeuLysPheHisIle 280
|||
DB 781 AAGACCCCATCTCTGCTTGTCTATGAGCCTGATGAATGGGGAGAGCTCAAGTTCCACATC 840
|||
QY 281 TyrAenValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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DB 841 TACAACTGGGCGACGCTGGCTGGACATGAGCGGGTGATCTTTTACTCGGCCAGATA 900
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QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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DB 901 GCCTGTGGATGCTGCACCTCATGAGCCTGATGAATGGGGAGAGCTCAAGTTCAGAGCTGAG 960
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QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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DB 961 AATGTGCTTCTGGATGACCTCGCAACCTGCAAGTTATCTGACCTGGGGCTGGCCCTGGAG 1020
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QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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DB 1021 ATGAAGGTGGCAAGCCCATCCCGAGAGGCTGGACCAATGGTTACTATGGCTCTGAG 1080
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QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
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DB 1081 ATCTAATGGGAAAGGTAAAGTTATCTCTATCTGTGGACTGTTTGGCCATGGGATGACG 1140
|||
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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DB 1141 ATTTATGAATGGTGTGGAGCAACCACTTCAAGAGATTCAAGGAAAGAGTTCAGTAAA 1200
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QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
Db 1201 GAGGATCTGAGCAAGAACTCTGCAAGACGAGGTCAATTCAGCATGATTAACCTTACA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
Db 1261 GAGGAAGCAAAAGATATTTCAGGCTCTTTGGCTTAAGAAACAGAGCAACGCTTAGGA 1320
QY 441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACCGATCAACTTCTCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
Db 1381 CGCTGGAGCTGGCTAATTCAGCCCATTTGTGCCAGACCTTCAGTGGTTTATGCC 1440
QY 481 LysAspIleAlaGluLeuAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db 1441 AAAGACATCGCTCAAAATTCATGATTTCTGAGGTTCCGGGGGTGGAATTTTCATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrrGlnGluGlu 520
Db 1501 GATAGACAGTTCTTCAAAACATTTGCGACAGGTGCTTCTTATAGCATGGCAGGAAGAA 1560
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATAGAAACGGGACTGTTTGGAGNACTGAATGATGCCCAACAGACCTACGGTTGTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGGTAAATTCATCAAGTCTGGCGTGTGTTGTTATTG 1659
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US-10-425-962-1
; Sequence 1, Application US/10425962
; Publication NO. US20030180786A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV2
; CURRENT APPLICATION NUMBER: US/10/425,962
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-425-962-1
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Alignment Scores:

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Pred. No.: 0 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 16 Gaps: 0
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US-10-044-205A-2 (1-553) x US-10-425-962-1 (1-1662)

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Db 1 ATGGTGGAGATGGGGGCCCTGGACAACTGATCGCAACACCGGCTACCTGAGGCCCGG 60
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QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 61 AAGCCCTCGGACTGGCAGCAGCAAGAGCTGCGGGCGCGGCTAGCTGGCCCTGGCCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGCAGGGCTGCGCGAGCTCCGCAGAAAGCTGTCCCTGAACTTCCACAGCCCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGCAGCCCATCGGTGCGCCCTCTTCGTGACTTCTTAGCCACAGTCCCACTGTC 240
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
Db 241 CGCAAGGGCGGCAACTTCTTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGAACC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAAGACAGCGCGCTGCAGGGCTGGTGCCACTTGTGCGAGTGCCTGCTGCCCGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCCGCAACCTTCTCAGCCAGCGGTGGCCACCAAGTCCCAAGCAGCAGCCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGAGCGAGTGGCTGCAGTGACCGTGGCCAAAGCTGAGGCCATGGCTTCTTTCGACAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGGATTTCTGACCAAGCGCTTCTACGACAAGTTCTTCAGTGGAAACTC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 601 GGTWTTGGGGAGGTATGTGCGCTCCAGTGAANAACACTGGGAAGATGTATGCTGTAAAG 660
QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGluLys 240
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QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db 721 GAAATCTTGGAAAGGTGAGCGCCCTTCAATGCTCTCTGCGCTATGCTCTTTGAGAGC 780
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Db 781 AAGACCCATCTCTGCTTGTGATGAGCTGATGAGCTGATGAGGAGACCTCAAGTTCACATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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QY 301 AlaCysGlyMetLeuHisGlnLeuGlyIleValTyrArgAspMetLysProGlu 320
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QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db 1021 ATGAAGGGTGGCAAGCCCATCCAGAGGGCTGGAACCAATGGTTTACATGGCTCTCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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RESULT 12

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; Sequence 273, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier, Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 273
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-273

Alignment Scores:
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Score: 2823.50 Matches: 547
Percent Similarity: 98.56% Conservative: 0
Best Local Similarity: 98.56% Mismatches: 1
Query Match: 97.73% Indels: 7
DB: 17 Gaps: 3

US-10-044-205A-2 (1-553) x US-10-072-012-273 (1-1701)
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Db 139 GGGCTGACGGCTCGCGGAGCTCGCCAGAAAGTGTCCCTGAACTTCCACAGCTGTGT 198
Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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Qy 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
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Qy 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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Qy 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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Db 439 GAAGAGCGAGTGGCTGCAGTGCAGCTGCAGGCTGAGGCGCATGGCTTCTTTCAGAGAG 498
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyAspLysPheLeuGlnTrpLysLeu 180
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Db 559 TTCGAGATGCAACACCAAGTGTTCAGACAGTACTTCACTGAGTTCAGAGTCTGGGNAAGGT 618
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2008.8	91.4	2249	US-10-217-745-5	Sequence 5, Appli
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5	1657.2	75.4	1662	US-09-738-894A-1	Sequence 1, Appli
6	1657.2	75.4	1662	US-09-964-469-1	Sequence 1, Appli
7	1046.8	47.6	1062	US-09-802-117-3	Sequence 3, Appli
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9	867.4	39.5	36651	US-09-738-894A-3	Sequence 3, Appli
10	867.4	39.5	36651	US-09-964-469-3	Sequence 3, Appli
11	419.8	19.1	2848	US-08-464-954A-2	Sequence 2, Appli
12	418.2	19.0	2204	US-08-221-817-12	Sequence 12, Appli
13	418.2	19.0	2204	US-08-454-439-12	Sequence 12, Appli
14	418.2	19.0	2204	PCT-US94-10487-10	Sequence 10, Appli
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22	373	17.0	2529	US-09-417-197-42	Sequence 42, Appli
23	373	17.0	2557	US-09-016-434-1298	Sequence 1298, Ap
24	366.6	16.7	2557	US-08-464-954A-1	Sequence 1, Appli
25	320.6	14.6	2017	US-09-614-748A-8	Sequence 8, Appli
26	320.6	14.6	2113	US-09-614-748A-7	Sequence 7, Appli
27	311.6	14.2	1879	US-09-614-748A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-09-802-117-5
; Sequence 5, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polyn
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-5

Query Match	91.4%	Score 2008.8;	DB 3;	Length 2249;
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			Gaps	0;
Qy	175	CAGGCCACAGGACTCAGCTGTAATCCCTTGGAGCTGTCTCACCCGGGAGGGAAGCAG	234	Sequence 1, Appli
Db	238	CAGGCCACAGGACTCAGCTGTAATCCCTTGGAGCTGTCTCACCCGGGAGGGAAGCAG	297	Sequence 1, Appli
Qy	235	CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCTGGAGTGGCCCGCTGCTCAGCCATGG	294	Sequence 3, Appli
Db	298	CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCTGGAGTGGCCCGCTGCTCAGCCATGG	357	Sequence 3, Appli
Qy	295	TGGACATGGGGCCCTTGACACACCTGATCGCCACACCGCTTACCTGACGGCCGGAGC	354	Sequence 3, Appli
Db	358	TGGACATGGGGCCCTTGACACACCTGATCGCCACACCGCTTACCTGACGGCCGGAGC	417	Sequence 3, Appli
Qy	355	CCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGGTAGCTGGCCCTCGCCCGGC	414	Sequence 10, Appli
Db	418	CCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGGTAGCTGGCCCTCGCCCGGC	477	Sequence 10, Appli
Qy	415	TGCAGGGCTGCGCGGAGCTCCGCCAGAGAGCTGTCCCTGAACCTTCCACAGCCTGTGTGAGC	474	Sequence 60, Appli
Db	478	TGCAGGGCTGCGCGGAGCTCCGCCAGAGAGCTGTCCCTGAACCTTCCACAGCCTGTGTGAGC	537	Sequence 1298, Ap
Qy	475	AGCAGCCCATCGTGGCGCCCTCTTCCGTGACTTCTTAGCCACAGTCCCGACGTTCCGCA	534	Sequence 8, Appli
Db	538	AGCAGCCCATCGTGGCGCCCTCTTCCGTGACTTCTTAGCCACAGTCCCGACGTTCCGCA	597	Sequence 7, Appli

QY 535 AGGGGCAACCTTCTAGAGGACGTGCAGAACTGGAGCTGGCCGAGGAGGACCCACCA 594
 Db 598 AGGGGCAACCTTCTAGAGGACGTGCAGAACTGGAGCTGGCCGAGGAGGACCCACCA 657
 QY 595 AAGCAGCGCGCTGCAGGGCTGTGGCCACTTGTGCGAGTGCCTGCCCGGGGAACC 654
 Db 658 AAGCAGCGCGCTGCAGGGCTGTGGCCACTTGTGCGAGTGCCTGCCCGGGGAACC 717
 QY 655 CGCAACCTTCTAGAGGACGTGCAGAACTGGAGCTGGCCGAGGAGGACCCACCA 714
 Db 718 CGCAACCTTCTAGAGGACGTGCAGAACTGGAGCTGGCCGAGGAGGACCCACCA 777
 QY 715 AGCGAGTGGCTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 774
 Db 778 AGCGAGTGGCTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 837
 QY 775 CTTTAAAGATTTCTGACGAGCGCTTCTACGACAACTTCTGAGTGCAGTGCAGTGCAG 834
 Db 838 CTTTAAAGATTTCTGACGAGCGCTTCTACGACAACTTCTGAGTGCAGTGCAGTGCAG 897
 QY 835 AGATCAACAGTGTGCAGAACTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 894
 Db 898 AGATCAACAGTGTGCAGAACTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 957
 QY 895 TTGGGAGGTATGTCCGCTCCAGGTGAAACACCTGGGAAAGATGATGCTGTGAAGAAC 954
 Db 958 TTGGGAGGTATGTCCGCTCCAGGTGAAACACCTGGGAAAGATGATGCTGTGAAGAAC 1017
 QY 955 TGGCAAGAAGCGGTGGAAGAAAGGTGGGAGAGATGGCTCTCTTGGAAAGGAAA 1014
 Db 1018 TGGCAAGAAGCGGTGGAAGAAAGGTGGGAGAGATGGCTCTCTTGGAAAGGAAA 1077
 QY 1015 TCTTGGAGAGTGCAGAGCGCTTCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1074
 Db 1078 TCTTGGAGAGTGCAGAGCGCTTCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1137
 QY 1075 CCATCTCTGCTTGTGATGACCTGATGAATGGGGAGACCTCAAGTTTCCACATCTACA 1134
 Db 1138 CCATCTCTGCTTGTGATGACCTGATGAATGGGGAGACCTCAAGTTTCCACATCTACA 1197
 QY 1135 AGTGGGACCGGTGGCTGGACATGAGCGGGGTGATCTTTACTCGGCCGAGATAGCT 1194
 Db 1198 AGTGGGACCGGTGGCTGGACATGAGCGGGGTGATCTTTACTCGGCCGAGATAGCT 1257
 QY 1195 GTGGAGTGTGACCTCCATGACCTCGCATCGTCTATCGGACATGAGCTGAGATG 1254
 Db 1258 GTGGAGTGTGACCTCCATGACCTCGCATCGTCTATCGGACATGAGCTGAGATG 1317
 QY 1255 TGCTTCTGGATGACCTCGGCAACTGCAGGTATCTGACCTGGGGCTGGCGTGGAGATGA 1314
 Db 1318 TGCTTCTGGATGACCTCGGCAACTGCAGGTATCTGACCTGGGGCTGGCGTGGAGATGA 1377
 QY 1315 AGGTGGCAAGCCATFACCCAGAGGCTGGAAACCAATGGTTTACATGGCTCTGAGATCC 1374
 Db 1378 AGGTGGCAAGCCATFACCCAGAGGCTGGAAACCAATGGTTTACATGGCTCTGAGATCC 1437
 QY 1375 TAAAGGAAAGTAAAGTTATCTTCTGCTGAGCTGGTTTGGCATGGGATGACATTT 1434
 Db 1438 TAAAGGAAAGTAAAGTTATCTTCTGCTGAGCTGGTTTGGCATGGGATGACATTT 1497
 QY 1435 ATGAATGTTGCTGGCAAGCAACCACTTCAAGAGATTTCAAGGAAAGGTTCAGTAAAGAGG 1494
 Db 1498 ATGAATGTTGCTGGCAAGCAACCACTTCAAGAGATTTCAAGGAAAGGTTCAGTAAAGAGG 1557
 QY 1495 ATCTGAAGCAAGACTCTGCAAGAGGAGTCAATTCAGCATGATGATTAATTCAGAGG 1554
 Db 1558 ATCTGAAGCAAGACTCTGCAAGAGGAGTCAATTCAGCATGATGATTAATTCAGAGG 1617
 QY 1555 AAGCAAGATATTTTCAGGCTCTTCTGCTTAAAGAAACAGAGCAAGCTTTAGGAAGCA 1614
 Db 1618 AAGCAAGATATTTTCAGGCTCTTCTGCTTAAAGAAACAGAGCAAGCTTTAGGAAGCA 1677

QY 1615 GAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAAAACGATCAACTTTCTCGCC 1674
 Db 1678 GAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAAAACGATCAACTTTCTCGCC 1737
 QY 1675 TGGAGCTGGCTTAATGAAACCCCATTTGTCAGACCCCTTCAGTGTGTTTATGCCAAAG 1734
 Db 1738 TGGAGCTGGCTTAATGAAACCCCATTTGTCAGACCCCTTCAGTGTGTTTATGCCAAAG 1797
 QY 1735 ACATCGCTGAAATTTGATGATTTCTCTGAGGTTCGGGGGTGGAAATTTGATGACAAAGATA 1794
 Db 1798 ACATCGCTGAAATTTGATGATTTCTCTGAGGTTCGGGGGTGGAAATTTGATGACAAAGATA 1857
 QY 1795 AGCAGTTCTTCAAAAACCTTTGCGACAGGTGTGTTCTATAGCATGGCAGGAAAGAAATTA 1854
 Db 1858 AGCAGTTCTTCAAAAACCTTTGCGACAGGTGTGTTCTATAGCATGGCAGGAAAGAAATTA 1917
 QY 1855 TAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTTACGGTTGTGAGGAGG 1914
 Db 1918 TAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTTACGGTTGTGAGGAGG 1977
 QY 1915 GTAATTCATCAAGTCTGGGGTGTGTTTGTATTTGTAATTTGCTCTCTTTACCCAGACAGG 1974
 Db 1978 GTAATTCATCAAGTCTGGGGTGTGTTTGTATTTGTAATTTGCTCTCTTTACCCAGACAGG 2037
 QY 1975 CAGCAGAGTCTCGGCTGACATAATCTCTGATGTTTCCACAGCTGGAAATCTGTGGATG 2034
 Db 2038 CAGCAGAGTCTCGGCTGACATAATCTCTGATGTTTCCACAGCTGGAAATCTGTGGATG 2097
 QY 2035 AGGCTAATCAGTTAGAGGGACATCAACCAACAAACAAATTCAAAAGACAGGCAAGCT 2094
 Db 2098 AGGCTAATCAGTTAGAGGGACATCAACCAACAAACAAATTCAAAAGACAGGCAAGCT 2157
 QY 2095 CACTACTAGAACACATTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2154
 Db 2158 CACTACTAGAACACATTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2217
 QY 2155 TTTTCTAGAGGAGGAGGAAAGAACTCA 2186
 Db 2218 TTTTCTAGAGGAGGAGGAAAGAACTCA 2249

RESULT 2

US-10-217-745-5
 ; Sequence 5, Application US/10217745
 ; Patent No. 6838275
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
 ; TITLE OF INVENTION: Polynucleotides
 ; TITLE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT APPLICATION NUMBER: US/10/217,745
 ; CURRENT FILING DATE: 2002-08-12
 ; PRIOR APPLICATION NUMBER: US/09/802,117
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 2249
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-217-745-5

Query Match 91.4%; Score 2008.8; DB 4; Length 2249;
 Best Local Similarity 99.9%; Pred No. 0;
 Matches 2010; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 175 CAGGCCACAGGACTCACTGTAATCCCTTGGAGCTGTCTACCCGGGAAAGGAAAGCAG 234
 Db 238 CAGGCCACAGGACTCACTGTAATCCCTTGGAGCTGTCTACCCGGGAAAGGAAAGCAG 297

QY 235 CCAGCAGCCCTCCAGCCCTCTTGTGCTTCCCTGGAGTGCSCCGGCTGCTCAGCATGG 294
Db 298 CCAGCAGCCCTCCAGCCCTCTTGTGCTTCCCTGGAGTGCSCCGGCTGCTCAGCATGG 357
QY 295 TGGACATGGGGCCCTGGACAACTGATCGCCAAACACAGCCCTACCTGAGAGCCCGGAGC 354
Db 358 TGGACATGGGGCCCTGGACAACTGATCGCCAAACACAGCCCTACCTGAGAGCCCGGAGC 417
QY 355 CTTGGACTGCGACAGCAAGAGCTGACAGCGCGCGGCGTACGCTGCGCCCTGCGCCGGGC 414
Db 418 CTTGGACTGCGACAGCAAGAGCTGACAGCGCGCGGCGTACGCTGCGCCCTGCGCCGGGC 477
QY 415 TGCAGGGCTGCGGGAGCTCCGCGAAGAGCTGCTCCTGNACTTCCACAGCCTGTGTGAGC 474
Db 478 TGCAGGGCTGCGGGAGCTCCGCGAAGAGCTGCTCCTGNACTTCCACAGCCTGTGTGAGC 537
QY 475 AGCAGCCATCGGTGCGCCCTCTTCCGTGACTTCTAGCCACAGTGCACGCTTCCGCA 534
Db 538 AGCAGCCATCGGTGCGCCCTCTTCCGTGACTTCTAGCCACAGTGCACGCTTCCGCA 597
QY 535 AGCGGCAACCTTCTAGAGGAGCTGCAGAACTGGGAGCTGGCGAGGAGGACCCACCA 594
Db 598 AGCGGCAACCTTCTAGAGGAGCTGCAGAACTGGGAGCTGGCGAGGAGGACCCACCA 657
QY 595 AAGACAGCGCTGACGGGCTGTGTGCGCACTTGTGCGAGTGCCTGCGCCCGGGGAACC 654
Db 658 AAGACAGCGCTGACGGGCTGTGTGCGCACTTGTGCGAGTGCCTGCGCCCGGGGAACC 717
QY 655 CGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGCACAGCCACCACTGAGGAAG 714
Db 718 CGCAACCTTCTCAGCAGCGCGTGGCCACCAAGTGCACAGCCACCACTGAGGAAG 777
QY 715 AGCAGTGGCTGACGTGCGCAAGGCTGAGGCCATGGCTTCTTCAAGAGCAGC 774
Db 778 AGCAGTGGCTGACGTGCGCAAGGCTGAGGCCATGGCTTCTTCAAGAGCAGC 837
QY 775 CTTTAAAGATTTCTGACAGCGCTTCTACGAAAGTTCTGAGTGGGAACTCTTCG 834
Db 838 CTTTAAAGATTTCTGACAGCGCTTCTACGAAAGTTCTGAGTGGGAACTCTTCG 897
QY 835 AGATGCAACAGTGTGACAGAGTACTTCACTGAGTTCAGAGTTCAGAGTGGGAAAGTGT 894
Db 898 AGATGCAACAGTGTGACAGAGTACTTCACTGAGTTCAGAGTTCAGAGTGGGAAAGTGT 957
QY 895 TTGGGAGGTATGTGCGCTCAGGTGAAAGAACACTGGGAAGATGATGCTGTGAAGAAC 954
Db 958 TTGGGAGGTATGTGCGCTCAGGTGAAAGAACACTGGGAAGATGATGCTGTGAAGAAC 1017
QY 955 TGGACAAAGCGGCTGAAGAAAGAGTGGCGAGAAATGCTCTTGGGAAAGGAAA 1014
Db 1018 TGGACAAAGCGGCTGAAGAAAGAGTGGCGAGAAATGCTCTTGGGAAAGGAAA 1077
QY 1015 TCTTGGAGAGGTGACAGCCCTTCACTGCTCTCTGCGCTATGCTTGGAGCAGA 1074
Db 1078 TCTTGGAGAGGTGACAGCCCTTCACTGCTCTCTGCGCTATGCTTGGAGCAGA 1137
QY 1075 CCCATCTCTGCTGCTATGAGCTGATGAATGGGGAGACCTCAAGTTCCACATCTACA 1134
Db 1138 CCCATCTCTGCTGCTATGAGCTGATGAATGGGGAGACCTCAAGTTCCACATCTACA 1197
QY 1135 ACGTGGGACCGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCACCATAGCCT 1194
Db 1198 ACGTGGGACCGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCACCATAGCCT 1257
QY 1195 GTGGATGCTGCACCTCCATGAACTCGGCATGCTCTATCGGACATGAAGCTGAGATG 1254
Db 1258 GTGGATGCTGCACCTCCATGAACTCGGCATGCTCTATCGGACATGAAGCTGAGATG 1317
QY 1255 TGCTTCTGATGACCTCGGCAACTGAGTTATCTGACTGGGCTGCGCGTGGAGATGA 1314
Db 1318 TGCTTCTGATGACCTCGGCAACTGAGTTATCTGACTGGGCTGCGCGTGGAGATGA 1377
QY 1315 AGGTTGGCAAGCCCATCCAGAGGGCTGGAAACCAATGGTTTACATGCTCTCTGAGATCC 1374

Db 1378 AGGTTGGCAAGCCCATCCAGAGGGCTGGAAACCAATGGTTTACATGCTCTCTGAGATCC 1437
QY 1375 TAAATGAAAAAGTAAAGTTATCTCTATCTGTGAGCTGGTTTGGCCATGGGATCGAGCATTT 1434
Db 1438 TAAATGAAAAAGTAAAGTTATCTCTATCTGTGAGCTGGTTTGGCCATGGGATCGAGCATTT 1497
QY 1435 ATGAAATGGTTGCTGGACGAAACACATTTCAAAGATTACAAGAAAGAGTCACTAAAGAGG 1494
Db 1498 ATGAAATGGTTGCTGGACGAAACACATTTCAAAGATTACAAGAAAGAGTCACTAAAGAGG 1557
QY 1495 ATCTGAAGCAAGAGTCTGCAAGCAGAGTCAAAATCCAGCATGATTAATCTTCAAGAGG 1554
Db 1558 ATCTGAAGCAAGAGTCTGCAAGCAGAGTCAAAATCCAGCATGATTAATCTTCAAGAGG 1617
QY 1555 AAGCAAAAGATATTTGCAAGGCTCTTCTTGGCTTAAGAAACAGAGCAACCGCTTGAAGACA 1614
Db 1618 AAGCAAAAGATATTTGCAAGGCTCTTCTTGGCTTAAGAAACAGAGCAACCGCTTGAAGACA 1677
QY 1615 GAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTTCTCGCC 1674
Db 1678 GAGAAAGTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTTCTCGCC 1737
QY 1675 TGGAGCTGGCTTAATTTGAACCCCAATTTTGGCCAGACCTTCACTGTTTATGCAAG 1734
Db 1738 TGGAGCTGGCTTAATTTGAACCCCAATTTTGGCCAGACCTTCACTGTTTATGCAAG 1797
QY 1735 ACATCGCTGAAATTTGATGATTTCTGAGGTTTGGGGGTTGGAATTTGATGACAAAGATA 1794
Db 1798 ACATCGCTGAAATTTGATGATTTCTGAGGTTTGGGGGTTGGAATTTGATGACAAAGATA 1857
QY 1795 AGCAGTCTTCAAAAACCTTTGCGACAGTGTCTTCTATAGCATGGCAGGAAGAAATTA 1854
Db 1858 AGCAGTCTTCAAAAACCTTTGCGACAGTGTCTTCTATAGCATGGCAGGAAGAAATTA 1917
QY 1855 TAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGTTGTGAGGAG 1914
Db 1918 TAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGTTGTGAGGAG 1977
QY 1915 GTAATTCATCAAGTCTGCGCTGCTGTTTGTATTGTTAAATGCTCTCTTTACACAGAG 1974
Db 1978 GTAATTCATCAAGTCTGCGCTGCTGTTTGTATTGTTAAATGCTCTCTTTACACAGAG 2037
QY 1975 CAGCAGGAGTCTCGGCTGACATAATCTCGAATGTTTCCACAGCTGGAAATCTGTGGAATG 2034
Db 2038 CAGCAGGAGTCTCGGCTGACATAATCTCGAATGTTTCCACAGCTGGAAATCTGTGGAATG 2097
QY 2035 AGGCTAATCAAGTTAGGAGGACATCAACCAAAACAAATTTCAAAAGACAGGCAAGCT 2094
Db 2098 AGGCTAATCAAGTTAGGAGGACATCAACCAAAACAAATTTCAAAAGACAGGCAAGCT 2157
QY 2095 CACTACTAGAACACATTTTATTTCTTTTCTTCTTCAAAAGATGATTAAGTCTCAG 2154
Db 2158 CACTACTAGAACACATTTTATTTCTTTCTTCTTCTTCAAAAGATGATTAAGTCTCAG 2217
QY 2155 TTTTCACTGAGGCGAGGAAAGGAACTCA 2186
Db 2218 TTTTCACTGAGGCGAGGAAAGGAACTCA 2249

RESULT 3

US-09-802-117-1
; Sequence 1, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polynu
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-1

Query Match 75.5%; Score 1658.4; DB 3; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGTGGACATGGGGGCTCGCAAACTGATCGCCAAACAGCGCTTACTCGAGGCCGG 350
Db 1 ATGTGGACATGGGGGCTCGCAAACTGATCGCCAAACAGCGCTTACTCGAGGCCGG 60

QY 351 AAGCCCTCGGACTGGACAGCAAGAGCTGAGCGGGCGGCGTAGCCTGGCCCTGCC 410
Db 61 AAGCCCTCGGACTGGACAGCAAGAGCTGAGCGGGCGGCGTAGCCTGGCCCTGCC 120

QY 411 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
Db 121 GGGCTGCAAGGCTGCGCGAGCTCGCGCAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

QY 471 GAGCAGCAGCCCATCGGTGCGCGCTCTTCGTGACTTCTAGCCACAGTGCACAGTTC 530
Db 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCGTGACTTCTAGCCACAGTGCACAGTTC 240

QY 531 CSCAAGGGGCAACTTCTTAGCAGAGCTGAGAACTGGAGCTGGCGAGGAGGAGGCC 590
Db 241 CSCAAGGGGCAACTTCTTAGCAGAGCTGAGAACTGGAGCTGGCGAGGAGGAGGCC 300

QY 591 ACCAAGACAGCGCTGAGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 650
Db 301 ACCAAGACAGCGCTGAGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 360

QY 651 AACCGCAACCTTCTGAGCAGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 710
Db 361 AACCGCAACCTTCTGAGCAGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 420

QY 711 GAAGAGCAGTGGCTGAGTGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 770
Db 421 GAAGAGCAGTGGCTGAGTGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 480

QY 771 CAGCCCTTTAAGATTTCTGACCAAGCTTCTGACCAAGCTTCTGACCAAGCTTCTGAC 830
Db 481 CAGCCCTTTAAGATTTCTGACCAAGCTTCTGACCAAGCTTCTGACCAAGCTTCTGAC 540

QY 831 TTGAGATGCAACCGCTGAGCAGTACTTCACTGAGTCTGAGTCTGAGTCTGAGTCTGAG 890
Db 541 TTGAGATGCAACCGCTGAGCAGTACTTCACTGAGTCTGAGTCTGAGTCTGAGTCTGAG 600

QY 891 GGTGTTGGGAGTATGTGCTGCTGAGTGAAGGCTGAGTGAAGGCTGAGTGAAGGCTGAG 950
Db 601 GGTGTTGGGAGTATGTGCTGCTGAGTGAAGGCTGAGTGAAGGCTGAGTGAAGGCTGAG 660

QY 951 AAATCGGCAAGAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1010
Db 661 AAATCGGCAAGAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720

QY 1011 GAAATCTTGGAGAGTGCAGGCTTTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 1070
Db 721 GAAATCTTGGAGAGTGCAGGCTTTCATTTCTGCTGCTGCTGCTGCTGCTGCTGAGG 780

QY 1071 AAGACCCATCTCTGCTTGTGATGAGCTGATGATGAGGAGGAGGAGGAGGAGGAGGAGG 1130
Db 781 AAGACCCATCTCTGCTTGTGATGAGCTGATGATGAGGAGGAGGAGGAGGAGGAGGAGG 840

QY 1131 TACAACTGGGCAAGGCTGCGCTGAGCAGTGGGCTGAGTCTTTTACTCGGCCAGATA 1190
Db 841 TACAACTGGGCAAGGCTGCGCTGAGCAGTGGGCTGAGTCTTTTACTCGGCCAGATA 900

QY 1191 GCCTGTGGGATGCTGCACCTCCATGAACCTCGCATCGTCTATCGGACATGAACCTGAG 1250
Db 901 GCCTGTGGGATGCTGCACCTCCATGAACCTCGCATCGTCTATCGGACATGAACCTGAG 960

QY 1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTATCTGACCTGGGGCTGGCGTGGAG 1310
Db 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAAGTATCTGACCTGGGGCTGGCGTGGAG 1020

QY 1311 ATGAGGGTGGCAAGCCCATCAACCCAGAGGCTGGACCAATGTTACATGCTTCCTGAG 1370
Db 1021 ATGAGGGTGGCAAGCCCATCAACCCAGAGGCTGGACCAATGTTACATGCTTCCTGAG 1080

QY 1371 ATCCTAATGAAAAGGTAAAGTATTTCTTATCTGCTGAGCTGGTTTGGCATGGGATGAGC 1430
Db 1081 ATCCTAATGAAAAGGTAAAGTATTTCTTATCTGCTGAGCTGGTTTGGCATGGGATGAGC 1140

QY 1431 ATTTATGAAATGTTGCTGAGCAACCAATTTCAAGATTACAGGAAAGGTGAGTAA 1490
Db 1141 ATTTATGAAATGTTGCTGAGCAACCAATTTCAAGATTACAGGAAAGGTGAGTAA 1200

QY 1491 GAGGATCTGAGCAAGAACTCTGCAAGAGAGGTCAAATTTCCAGCATGATACTTACA 1550
Db 1201 GAGGATCTGAGCAAGAACTCTGCAAGAGAGGTCAAATTTCCAGCATGATACTTACA 1260

QY 1551 GAGGAGCAAAAGATATTTGCAAGCTCTTCTTGGCTAAGAAACAGAGCAACGCTTAGGA 1610
Db 1261 GAGGAGCAAAAGATATTTGCAAGCTCTTCTTGGCTAAGAAACAGAGCAACGCTTAGGA 1320

QY 1611 AGCAGAGAAAGTCTGATGATCCAGGAAACATCTTTTAAACGATCAACTTTTCT 1670
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCTTTTAAACGATCAACTTTTCT 1380

QY 1671 CGCTGGAAGCTGCGCTAAATTTGAACCCCTTCTGTCAGACCCCTTCACTGCTTATGCC 1730
Db 1381 CGCTGGAAGCTGCGCTAAATTTGAACCCCTTCTGTCAGACCCCTTCACTGCTTATGCC 1440

QY 1731 AAAGACATCGTGAATTTGATGATTTCTCTGAGGTTGGGGGGTGGAAATTTGATGACAAA 1790
Db 1441 AAAGACATCGTGAATTTGATGATTTCTCTGAGGTTGGGGGGTGGAAATTTGATGACAAA 1500

QY 1791 GATAGCAGTTCTTCAAAACTTTGCGACAGTCTGTTCTCTATAGCATGCGAGGAGAA 1850
Db 1501 GATAGCAGTTCTTCAAAACTTTGCGACAGTCTGTTCTCTATAGCATGCGAGGAGAA 1560

QY 1851 ATTATAGAAACGGGACTGTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
Db 1561 ATTATAGAAACGGGACTGTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

QY 1911 GAGGTAATTCATCAAGCTGCGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1952
Db 1621 GAGGTAATTCATCAAGCTGCGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1662

RESULT 4

US-10-217-745-1
; Sequence 1, Application US/10217745
; Patent No. 6838275
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6838275el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

Qy	291	ATGTTGACATG	GGGGGCCCTGG	ACAACCTGATCG	CCAAACCGCCTAC	TCTGACGGCCCGG	350
Db	1	ATGTTGACATG	GGGGGCCCTGG	ACAACCTGATCG	CCAAACCGCCTAC	TCTGACGGCCCGG	60
Qy	351	AAGCCCTCG	ACATGCGACAG	CAAGAGCTGC	ACGGCGCGCGT	AGCTAGCCCTGGCCCTG	410
Db	61	AAGCCCTCG	ACATGCGACAG	CAAGAGCTGC	ACGGCGCGCGT	AGCTAGCCCTG	120
Qy	411	GGGCTGAGG	GCTCGCGGAGCT	CCGCGCAGAAG	CTGCCCTGAACTT	CCACAGCCTGTGT	470
Db	121	GGGCTGAGG	GCTCGCGGAGCT	CCGCGCAGAAG	CTGCCCTGAACTT	CCACAGCCTGTGT	180
Qy	471	GAGCAGAGC	CCATCGTTCGCG	CCCTCTTCGTCG	ACTTCTCTAGCCA	CAGTGCACCGTTC	530
Db	181	GAGCAGAGC	CCATCGTTCGCG	CCCTCTTCGTCG	ACTTCTCTAGCCA	CAGTGCACCGTTC	240
Qy	531	CGAAGCGCA	ACCTTCCTAG	AGGAGCTGC	AGAACTGGGAG	CTGGCCGAGGAGG	590
Db	241	CGAAGCGCA	ACCTTCCTAG	AGGAGCTGC	AGAACTGGGAG	CTGGCCGAGGAGG	300
Qy	591	ACCAAAGAC	GAGCGCGCTCG	AGGGGCGCTGG	TGGCCACTTGTG	CGAGTGCCCTG	650
Db	301	ACCAAAGAC	GAGCGCGCTCG	AGGGGCGCTGG	TGGCCACTTGTG	CGAGTGCCCTG	360
Qy	651	AACCCGCAA	CCCTTCTC	TAGCCAGCG	CGTGCCACCAAG	TGCCAAGCAGCA	710
Db	361	AACCCGCAA	CCCTTCTC	TAGCCAGCG	CGTGCCACCAAG	TGCCAAGCAGCA	420
Qy	711	GAAGAGCG	AGTGCGCTCAG	TGACGCTCGG	CNAGGCTGAGGCC	ATGCTTTCTTGC	770
Db	421	GAAGAGCG	AGTGCGCTCAG	TGACGCTCGG	CNAGGCTGAGGCC	ATGCTTTCTTGC	480
Qy	771	CAGCCCTTT	AAGGATTTCTG	TACCAAGCTTCT	TACCAAGCTTCT	TGCAAGTGGAACTC	830
Db	481	CAGCCCTTT	AAGGATTTCTG	TACCAAGCTTCT	TACCAAGCTTCT	TGCAAGTGGAACTC	540
Qy	831	TTCGAGATC	CAACCAAGTGT	CAGACAAGTA	CTTCACTGAGTGT	TCAGAGTGTGGGAAAGGT	890
Db	541	TTCGAGATC	CAACCAAGTGT	CAGACAAGTA	CTTCACTGAGTGT	TCAGAGTGTGGGAAAGGT	600
Qy	891	GGTTTTGGG	AGGTATGTCG	CGCTCCAGGTG	NAAACTGGGAG	ATGATGCTGTGAAG	950
Db	601	GGTTTTGGG	AGGTATGTCG	CGCTCCAGGTG	NAAACTGGGAG	ATGATGCTGTGAAG	660
Qy	951	AAACTGCA	AGAAAGCGGCT	GAAGAAAGGT	GGCGAGAGATGG	CTCTTTGGAAAG	1010
Db	661	AAACTGCA	AGAAAGCGGCT	GAAGAAAGGT	GGCGAGAGATGG	CTCTTTGGAAAG	720
Qy	1011	GAATCTTGG	AAGAGGT	CAGAGCCCTTT	CATTGTCTCT	CTGGCCTATGCTTTGAG	1070
Db	721	GAATCTTGG	AAGAGGT	CAGAGCCCTTT	CATTGTCTCT	CTGGCCTATGCTTTGAG	780
Qy	1071	AAGACCAT	CTCTGCTTTG	CATGAGCCTG	ATGAACTGGGG	GAGACCTCAAGTCC	1130
Db	781	AAGACCAT	CTCTGCTTTG	CATGAGCCTG	ATGAACTGGGG	GAGACCTCAAGTCC	840
Qy	1131	TACAACTGG	SGCAGCGCTGG	CGCTGGACA	TGAGCCGGGTG	ATCTTTTACTCGGCC	1190
Db	841	TACAACTGG	SGCAGCGCTGG	CGCTGGACA	TGAGCCGGGTG	ATCTTTTACTCGGCC	900
Qy	1191	GCCTGTGG	ATGCTGCACCT	CCATGAACT	CGGCATCGTCT	ATCGGAGACATGAAG	1250
Db	901	GCCTGTGG	ATGCTGCACCT	CCATGAACT	CGGCATCGTCT	ATCGGAGACATGAAG	960
Qy	1251	AATGTGCTT	CTGATGACCT	CGGCAACT	GCAGGTTATCT	GACCTGGGGCTGG	1310
Db	961	AATGTGCTT	CTGATGACCT	CGGCAACT	GCAGGTTATCT	GACCTGGGGCTGG	1020
Qy	1311	ATGAAGG	TGCAAGCCCAT	CACCCAGAG	GGCTGGAACCAAT	TGTTACATGGCT	1370
Db	1021	ATGAAGG	TGCAAGCCCAT	CACCCAGAG	GGCTGGAACCAAT	TGTTACATGGCT	1080
Qy	1371	ATCCTAAT	TGAAAAAG	GTAAAGTTAT	TCTCTATCCT	TGTGACCTGGTT	1430

1081	Db	ATCCTAATCGGAAGAAGTAGTTATTTCCTATCTCTGGAGCTGTTTGGCCATGGGATGTCAGC	1140
1431	Qy	ATTATTGAAATGGTTGCTGGACGAACACCATTTCAAAGATTACAAGAAAAAGTCAGTAAA	1490
1141	Db	ATTATTGAAATGGTTGCTGGACGAACACCATTTCAAAGATTACAAGAAAAAGTCAGTAAA	1200
1491	Qy	GAGGATCTGAAGAAAGAAACTCTGCAAGACGAGGTCAAATTTCCAGCATGATACTTCACA	1550
1201	Db	GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTTCCAGCATGATACTTCACA	1260
1551	Qy	GAGGAAGCAAAAAGATATTGTGCAGGCTCTCTTGGCTTAAGAAACCAAGACCAACGCTTAGGA	1610
1261	Db	GAGGAAGCAAAAAGATATTGTGCAGGCTCTCTTGGCTTAAGAAACCAAGACCAACGCTTAGGA	1320
1611	Qy	AGCAGAGAAAAGTCTGATGATCCCAGGAAACAATTTCTTTTAAACCGATCAACTTTGCT	1670
1321	Db	AGCAGAGAAAAGTCTGATGATCCCAGGAAACAATTTCTTTTAAACCGATCAACTTTGCT	1380
1671	Qy	CGCTCGGAAGCTGGCTTAATGAAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC	1730
1381	Db	CGCTCGGAAGCTGGCTTAATGAAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC	1440
1731	Qy	AAAGACATCGCTCAAAATTTGATGATTTCTCGAGGTTCGGGGGTGGAAATTTGATGACAAA	1790
1441	Db	AAAGACATCGCTGAAATTTGATGATTTCTCGAGGTTCGGGGGTGGAAATTTGATGACAAA	1500
1791	Qy	GATAGCAGTTCTTCAAAAACCTTTGGGACAGGTGCTGTTCTCTATAGCATGGCAGGAAGAA	1850
1501	Db	GATAGCAGTTCTTCAAAAACCTTTGGGACAGGTGCTGTTCTCTATAGCATGGCAGGAAGAA	1560
1851	Qy	ATTATAGAAAACGGGACTGTTTTCAGGAACTGAATGATCCCCAACAGACCTTACGGGTGTGAG	1910
1561	Db	ATTATAGAAAACGGGACTGTTTTCAGGAACTGAATGATCCCCAACAGACCTTACGGGTGTGAG	1620
1911	Qy	GAGGGTAATTCATCCAAAGTCTCGCGTGTGTTGTTTATTGTAA	1952
1621	Db	GAGGGTAATTCATCCAAAGTCTCGCGTGTGTTGTTTATTGTAA	1662

RESULT 6

```

US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1

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	Query Match	75.4%	Score 1557.2	DB 4	Length 1662
	Best Local Similarity	99.8%	Pred. No. 0		
	Matches 1659	Conservative	Mismatches 0	Indels 3	Gaps 0
QY	291	ATGTGGACATGGGGCCCTGGACAACCTGATCGCCACACACGGCTACTGTGAGCCCGG	350		
DB	1	ATGTGGACATGGGGCCCTGGACAACCTGATCGCCACACACGGCTACTGTGAGCCCGG	60		
QY	351	AAGCCCTCGAGCTGGCGACAGCAAGAGCTGCAGCGCGCGCGCTAGCCTGTGCCCTGTGCC	410		

Db 61 ||||| AGCCCTCGGACTGCGACGACGAAAGAGCTGACGCGGGGGCGGTAGCCCTGGCCCTGCCCC 120
QY 411 GGGCTGAGGGCTGGCGGAGCTCCGCCAGAAAGCTGTCCCTGAACTTCCACACGCTGTGT 470
Db 121 GGGCTGAGGGCTGGCGGAGCTCCGCCAGAAAGCTGTCCCTGAACTTCCACACGCTGTGT 180
QY 471 GAGCAGACCCCATCGGTGCGCGGCTTTCCTGCTGACTTCTAGCCACAGTGCCACGTTTC 530
Db 181 GAGCAGACCCCATCGGTGCGCGGCTTTCCTGCTGACTTCTAGCCACAGTGCCACGTTTC 240
QY 531 CGCAAGCGCGCAACCTTCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCC 590
Db 241 CGCAAGCGCGCAACCTTCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCC 300
QY 591 ACCAAAGACAGCGCTGACAGGGCTGGTGGCCACTTGTCCGAGTGCCCTGCCCCGGGG 650
Db 301 ACCAAAGACAGCGCTGACAGGGCTGGTGGCCACTTGTGGAGTGCCCTGCCCCGGGG 360
QY 651 AACCCGCAACCTTCTGACGAGCGCTGCGCAAGGCTGAGCCATGSCCTTCTTGCAGAG 710
Db 361 AACCCGCAACCTTCTGACGAGCGCTGCGCAAGGCTGAGCCATGSCCTTCTTGCAGAG 420
QY 711 GAAGAGCGAGTGGCTGAGTGCAGCGCTGCGCAAGGCTGAGCCATGSCCTTCTTGCAGAG 770
Db 421 GAAGAGCGAGTGGCTGAGTGCAGCGCTGCGCAAGGCTGAGCCATGSCCTTCTTGCAGAG 480
QY 771 CAGCCCTTTAAGGATTTCTGACGAGCGCTTCTACGACAAAGTTCTGCAAGTGGAACTC 830
Db 481 CAGCCCTTTAAGGATTTCTGACGAGCGCTTCTACGACAAAGTTCTGCAAGTGGAACTC 540
QY 831 TTCGAGATGCAACGAGTGCAGAAAGTCTTCACTGAGTTCAGAGTGTGGGGAAAGT 890
Db 541 TTCGAGATGCAACGAGTGCAGAAAGTCTTCACTGAGTTCAGAGTGTGGGGAAAGT 600
QY 891 GGTTTTGGGAGTATGTCGGCTGCAGGTGAAACACCTGGGAAGATGATCCCTGTAG 950
Db 601 GGTTTTGGGAGTATGTCGGCTGCAGGTGAAACACCTGGGAAGATGATCCCTGTAG 660
QY 951 AAATGGACAAGAGCGCTGAGAAAGAGTGGCGAAGATGGCTCTCTTGGAAAG 1010
Db 661 AAATGGACAAGAGCGCTGAGAAAGAGTGGCGAAGATGGCTCTCTTGGAAAG 720
QY 1011 GAAATCTTGGAGAGTGCAGAGCGCTTCACTGTCTCTGCGCTATGCCCTTGGAGC 1070
Db 721 GAAATCTTGGAGAGTGCAGAGCGCTTCACTGTCTCTGCGCTATGCCCTTGGAGC 780
QY 1071 AAGACCCATCTGCTGCTGATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC 1130
Db 781 AAGACCCATCTGCTGCTGATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC 840
QY 1131 TACAACTGGGCAAGCGCTGGCATGACATGAGCGGGTATCTTTTACTCGGCCAGATA 1190
Db 841 TACAACTGGGCAAGCGCTGGCATGACATGAGCGGGTATCTTTTACTCGGCCAGATA 900
QY 1191 GCCTGTGGATGCTGCACCTCATGAATCGGCATCGTCTATCGGGACATGAAGCTGAG 1250
Db 901 GCCTGTGGATGCTGCACCTCATGAATCGGCATCGTCTATCGGGACATGAAGCTGAG 960
QY 1251 AATGTGCTTGGATGACCTCGCAACTGCAGGTTATCTGACCTGGGGTGGCGGTGAG 1310
Db 961 AATGTGCTTGGATGACCTCGCAACTGCAGGTTATCTGACCTGGGGTGGCGGTGAG 1020
QY 1311 ATGAAGGTGGCAAGCCATACCCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG 1370
Db 1021 ATGAAGGTGGCAAGCCATACCCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG 1080
QY 1371 ATCTAATGAAAGAGTAAATTTCTTATCTGTGAGTGGTTTCCATGGGATGCAGC 1430
Db 1081 ATCTAATGAAAGAGTAAATTTCTTATCTGTGAGTGGTTTCCATGGGATGCAGC 1140
QY 1431 ATTTATGAAATGGTGTGGAGCAACCAATTTCAAAGATTACAAGAAAGTCAATGATAA 1490
|||||

Db 1141 ATTTATGAAATGGTGTCTGCGAAGACCACTTCAAAGATTACAAGAAAGTCACTGATAA 1200
QY 1491 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTTCCAGATGATCACTTCA 1550
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAAATTTCCAGATGATCACTTCA 1260
QY 1551 GAGGAGCAAAAGATATTTGCAAGGCTTCTTGGCTAAGAAACAGACGACGCTTAGGA 1610
Db 1261 GAGGAGCAAAAGATATTTGCAAGGCTTCTTGGCTAAGAAACAGACGACGCTTAGGA 1320
QY 1611 AGCAGAGAAAGCTCTGATGATCCAGGAAACATATTTCTTTTAAACGATCAACTTTCCT 1670
Db 1321 AGCAGAGAAAGCTCTGATGATCCAGGAAACATATTTCTTTTAAACGATCAACTTTCCT 1380
QY 1671 CCGCTGGAGCTGGCTTAATGAACCCCAATTTGTGCCAGACCTTTCAGTGGTTTATGCC 1730
Db 1381 CCGCTGGAGCTGGCTTAATGAACCCCAATTTGTGCCAGACCTTTCAGTGGTTTATGCC 1440
QY 1731 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTGATGACAA 1790
Db 1441 AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAATTTGATGACAA 1500
QY 1791 GATAAGCAGTTCTTCAAAACCTTTGCGACAGGTGCTTCTTATAGCATGGCAGGAAGA 1850
Db 1501 GATAAGCAGTTCTTCAAAACCTTTGCGACAGGTGCTTCTTATAGCATGGCAGGAAGA 1560
QY 1851 ATTATAGAAACGGGACTGTTTGCAGAACTGAATGACCCCAACAGACCTACGGGTTCTGAG 1910
Db 1561 ATTATAGAAACGGGACTGTTTGCAGAACTGAATGACCCCAACAGACCTACGGGTTCTGAG 1620
QY 1911 GAGGTAATTCATCAAGTCTGGCGTGTGTTTGTATTGTAA 1952
Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTTGTATTGTAA 1662
|||||

RESULT 7

US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 644456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polyn
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3

Query Match 47.6%; Score 1046.8; DB 3; Length 1062;
Best Local Similarity 99.8%; Pred. No. 3.4e-258;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 291 ATGTGGACATGGGGGCCCTGGACAACTGATCGCAACACCGCTACTCTGAGGCGCCG 350
Db 1 ATGTGGACATGGGGGCCCTGGACAACTGATCGCAACACCGCTACTCTGAGGCGCCG 60
QY 351 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAAGCGCGCGGTAGCTGAGCTGAGCTGCCC 410
Db 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAAGCGCGCGGTAGCTGAGCTGAGCTGCCC 120
QY 411 GGGCTGAGGCGTGGCGGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGGCTGTGT 470
Db 121 GGGCTGAGGCGTGGCGGAGCTCGCCAGAAAGCTGTCCCTGAACTTCCACAGGCTGTGT 180
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Qy	471	GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTCCCAACGTTTC	530
Db	181	GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTCCCAACGTTTC	240
Qy	531	CGAAGCGGGCAACTCTTCTTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCC	590
Db	241	CGAAGCGGGCAACTCTTCTTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCC	300
Qy	591	ACCAAGACACGCGCTGACGGGGCTGGTGGCCACTTGTGCGAGTGCCTCTGCCCCCGGG	650
Db	301	ACCAAGACACGCGCTGACGGGGCTGGTGGCCACTTGTGCGAGTGCCTCTGCCCCCGGG	360
Qy	651	AACCCGCAACCTTCTCAGCCAGCCCGTGGCCACCAAGTGCCAAGCAGCACCACTGAG	710
Db	361	AACCCGCAACCTTCTCAGCCAGCCCGTGGCCACCAAGTGCCAAGCAGCACCACTGAG	420
Qy	711	GAAGACGAGTGGCTGCAGTGAACCTGCGCAAGGCTGAGGCCATGGCTTCTTGCACAG	770
Db	421	GAAGACGAGTGGCTGCAGTGAACCTGCGCAAGGCTGAGGCCATGGCTTCTTGCACAG	480
Qy	771	CAGCCCTTTAAGGATTTCTGACACAGCGCCTTCTACGACAAAGTTTCTCAGTGGAACTC	830
Db	481	CAGCCCTTTAAGGATTTCTGACACAGCGCCTTCTACGACAAAGTTTCTCAGTGGAACTC	540
Qy	831	TTCGAGATGC AACGAGTGTGCAGAAAGTACTTCTACTGATTCAGAGTCTCTGGGGAAGGT	890
Db	541	TTCGAGATGC AACGAGTGTGCAGAAAGTACTTCTACTGATTCAGAGTCTCTGGGGAAGGT	600
Qy	891	-GGTTTTCGGGAGGTATGCGCGTCCAGGTGAAACACTGCGGAAGATGATGTCCTGTAA	950
Db	601	GGTTTTCGGGAGGTATGCGCGTCCAGGTGAAACACTGCGGAAGATGATGTCCTGTAA	660
Qy	951	AAACTGGACAAGAGCGGCTGAAGAAAGAGTGGCGAGAAGATGGCTCTCTTGAAAG	1010
Db	661	AAACTGGACAAGAGCGGCTGAAGAAAGAGTGGCGAGAAGATGGCTCTCTTGAAAG	720
Qy	1011	GAATCTTTGGAGAGGTGAGAGCGCTTCAATGTTCTCTGCGCCTATGCTTTGAGAGC	1070
Db	721	GAATCTTTGGAGAGGTGAGAGCGCTTCAATGTTCTCTGCGCCTATGCTTTGAGAGC	780
Qy	1071	AAGACCCATCTGCTGTTGTCATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC	1130
Db	781	AAGACCCATCTGCTGTTGTCATGAGCTGATGAATGGGGAGACCTCAAGTTCACATC	840
Qy	1131	TACAACTGGGCACGCTGGCTTGGACATGAGCCGGGTGATCTTTTATCTCGGCCCAGATA	1190
Db	841	TACAACTGGGCACGCTGGCTTGGACATGAGCCGGGTGATCTTTTATCTCGGCCCAGATA	900
Qy	1191	GCCTGTGGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG	1250
Db	901	GCCTGTGGGATGCTGCACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG	960
Qy	1251	AATGTCTTCTGGATGACTCGGCAACTGACAGTTTATCTGACCTGGGCTGCGCCGTGAG	1310
Db	961	AATGTCTTCTGGATGACTCGGCAACTGACAGTTTATCTGACCTGGGCTGCGCCGTGAG	1020
Qy	1311	ATGAAGGCTGGCAAGCCCATCACCCAGAGG	1340
Db	1021	ATGAAGGCTGGCAAGCCCATCACCCAGAGG	1050

RESULT 8

[illegible]

QY 1131 TACAACTGGGACCGGTGGCTGACATGACCGGTGATCTTTTACTCGGCCAGATA 1190
DB 841 TACAACTGGGACCGGTGGCTGACATGACCGGTGATCTTTTACTCGGCCAGATA 900
QY 1191 GCCTGTGGGATGCTGCACCTCATGAACCTGCGCATGCTATCGGGACATGAAGCTGAG 1250
DB 901 GCCTGTGGGATGCTGCACCTCATGAACCTGCGCATGCTATCGGGACATGAAGCTGAG 960
QY 1251 AATGTCTTCTGGATGACCTCGGCAACTGCGAGTTTATCTGACCTGGGGCTGGCGTGGAG 1310
DB 961 AATGTCTTCTGGATGACCTCGGCAACTGCGAGTTTATCTGACCTGGGGCTGGCGTGGAG 1020
QY 1311 ATGAAGGTGGCAAGCCCATACCCAGAGG 1340
DB 1021 ATGAAGGTGGCAAGCCCATACCCAGAGG 1050

RESULT 9

US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

Query Match 39.5%; Score 867.4; DB 3; Length 36651;
Best Local Similarity 95.1%; Pred. No. 1.9e-211;
Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GACCCCTAAGATGAAGGACCTCACTATAGGCTCGAGCGCGCGCGGCGAGGTGTCACGACGCTTTC 60
DB 1786 GACCCCTAAGATGAAGGACCTCACTATAGGCTCGAGCGCGCGCGGCGAGGTGTCACGACGCTTTC 1845
QY 61 GCCTTGGCAGGTGGGACGATGACCTATCGTGTGACGTTCTCTGGCGGGCTATACATAGCCA 120
DB 1846 GCCTTGGCAGGTGGGACGATGACCTATCGTGTGACGTTCTCTGGCGGGCTATACATAGCCA 1905
QY 121 GTCAAAGCTTTTACAAAGAAACCTTTTACACCTTCCACGGGTGCCACCCACGAGCC 180
DB 1906 GTCAAAGCTTTTACAAAGAAACCTTTTACACCTTCCACGGGTGCCACCCACGAGCC 1965
QY 181 ACAGACTCACTGTAATCCCTTGGACGTTGTCTACCCGGGAAGGAAAGCAGCCAGCA 240
DB 1966 ACAGACTCACTGTAATCCCTTGGACGTTGTCTACCCGGGAAGGAAAGCAGCCAGCA 2025
QY 241 GCCTTCCAGCCCTCTTGTGCTTTCTCTGGAGTGGCGCCCGTGTCTACGACATGGTGACA 300
DB 2026 GCCTTCCAGCCCTCTTGTGCTTTCTCTGGAGTGGCGCCCGTGTCTACGACATGGTGACA 2085
QY 301 TGGGGGCGCTTGACAACTGTATGCGCAACACCGCCCTACCTGAGGCGCGGAAAGCCCTCGG 360
DB 2086 TGGGGGCGCTTGACAACTGTATGCGCAACACCGCCCTACCTGAGGCGCGGAAAGCCCTCGG 2145
QY 361 ACTGCGACAGCAAGAGCTGACGCGCGCGCGGTAGCTGCGCCCTGCGCCCGGCTGCGAGG 420
DB 2146 ACTGCGACAGCAAGAGCTGACGCGCGCGCGGTAGCTGCGCCCTGCGCCCGGCTGCGAGG 2205

QY 421 GCTGGCGGAGTCCGCCAGAAAGCTGTCCCTGAACCTTCCACAGCCTGTGTGAGCAGCAGC 480
DB 2206 GCTGGCGGAGTCCGCCAGAAAGCTGTCCCTGAACCTTCCACAGCCTGTGTGAGCAGCAGC 2265
QY 481 CCATCGGTGCGCGCTCTTTCCGTGACTTTCCTAGCCACAGTGCACAGTTCGCCCAAGGCGG 540
DB 2266 CCATCGGTGCGCGCTCTTTCCGTGACTTTCCTAGCCACAGTGCACAGTTCGCCCAAGGCGG 2325
QY 541 CAACCTTCTAGAGGACGTGCGAACTCGGAGCTGCGCGAGGAGGAGGCCACCAAGACA 600
DB 2326 CAACCTTCTAGAGGACGTGCGAACTCGGAGCTGCGCGAGGAGGAGGCCACCAAGACA 2385
QY 601 GCGCGCTCAGGCGCTGTGCGCACTTGTGCGAGTGCCTCTCCCGGGGAAACCCGCAAC 660
DB 2386 GCGCGCTCAGGCGCTGTGCGCACTTGTGCGAGTGCCTCTCCCGGGGAAACCCGCAAC 2445
QY 661 CCTTCTCAGCAGCGCGCTGCGCACTTGTGCGAGTGCCTCTCCCGGGGAAACCCGCAAC 720
DB 2446 CCTTCTCAGCAGCGCGCTGCGCACTTGTGCGAGTGCCTCTCCCGGGGAAACCCGCAAC 2505
QY 721 TGGCTGACGTGACGCTGCGCAAGGCTGAGGCGCATGGCTTTCTTCAAGAGCAGCCCTTTTA 780
DB 2506 TGGCTGACGTGACGCTGCGCAAGGCTGAGGCGCATGGCTTTCTTCAAGAGCAGCCCTTTTA 2565
QY 781 AGGATTTCTGACACAGCGCTTCTACGACAAAGTTTCTGAGTGGAACTCTTCGAGATGC 840
DB 2566 AGGATTTCTGACACAGCGCTTCTACGACAAAGTTTCTGAGTGGAACTCTTCGAGATGC 2625
QY 841 AACCAGTGTGACAGTACTTCACTGAGTTCAGAGTCTGGGAAAGTGGTTTGGGG 900
DB 2626 AACCAGTGTGACAGTACTTCACTGAGTTCAGAGTCTGGGAAAGTGGTTTGGGG 2685
QY 901 AGGTATGTGCGCTCCAGGTGAAACACTGCGGAAGATGTAT 941
DB 2686 AGGTATGTGCTCCAGTAGCCAGCTAGAGGTGAAGCAT 2726

RESULT 10

US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

Query Match 39.5%; Score 867.4; DB 4; Length 36651;
Best Local Similarity 95.1%; Pred. No. 1.9e-211;
Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GACCCCTAAGATGAAGGACCTCACTATAGGCTCGAGCGCGCGCGGCGAGGTGTCACGACGCTTTC 60
DB 1786 GACCCCTAAGATGAAGGACCTCACTATAGGCTCGAGCGCGCGCGGCGAGGTGTCACGACGCTTTC 1845

61 GCCTGGCAGGTGGGAGCATGACCTATCTGTGCGAGTTCTTGGGGGCTATACATAGCCA 120
Db
1846 GCCTGGCAGGTGGGAGCATGACCTATCTGTGCGAGTTCTTGGGGGCTATACATAGCCA 1905
Qy
121 GTCAAGGCTTTTCAAAAAGAACTCTTTTCAACCTTCCACGGGTCCACCCACAGGCC 180
Db
1906 GTCAAGGCTTTTCAAAAAGAACTCTTTTCAACCTTCCACGGGTCCACCCACAGGCC 1965
Qy
181 ACAGGACTCAGTGAATCCCTTGGAGCTTGTCTCACCCGGGAGGGAAGCAGCCAGCA 240
Db
1966 ACAGGACTCAGTGAATCCCTTGGAGCTTGTCTCACCCGGGAGGGAAGCAGCCAGCA 2025
Qy
241 GCCCTCCAGCCCTCTTGTGCTTCCCTGGAGTGGCCCGCTGTCTCAGCCATGGTGACA 300
Db
2026 GCCCTCCAGCCCTCTTGTGCTTCCCTGGAGTGGCCCGCTGTCTCAGCCATGGTGACA 2085
Qy
301 TGGGGCCCTTGACAACTGATGCGCAACCGGCTACTCTGAGGCCCGGAAGCCCTCGG 360
Db
2086 TGGGGCCCTTGACAACTGATGCGCAACCGGCTACTCTGAGGCCCGGAAGCCCTCGG 2145
Qy
361 ACTGCGACAGCAAGAGCTGCAGCGCGCGGCTAGCTGGCCCTGCGCGGCTGCAGG 420
Db
2146 ACTGCGACAGCAAGAGCTGCAGCGCGCGGCTAGCTGGCCCTGCGCGGCTGCAGG 2205
Qy
421 GCTGCGCGAGCTCGCGCAGAGCTGTCCCTGAACCTTCCACAGCTGTGTGAGCAGCAGC 480
Db
2206 GCTGCGCGAGCTCGCGCAGAGCTGTCCCTGAACCTTCCACAGCTGTGTGAGCAGCAGC 2265
Qy
481 CCATCGGTGGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTCGCGCAAGCGG 540
Db
2266 CCATCGGTGGCGCTCTTCCGTGACTTCTTAGCCACAGTGCACAGTTCGCGCAAGCGG 2325
Qy
541 CAACCTTCTTAGAGACAGTGCAGAGCTGGGAGCTGGCGAGGAGGACCCACCAAGACA 600
Db
2326 CAACCTTCTTAGAGACAGTGCAGAGCTGGGAGCTGGCGAGGAGGACCCACCAAGACA 2385
Qy
601 GGGCGCTGCAGGGCTGTGGCCACTTGTGAGTGGCCCTGCGCGGGGAAACCGCAAC 660
Db
2386 GGGCGCTGCAGGGCTGTGGCCACTTGTGAGTGGCCCTGCGCGGGGAAACCGCAAC 2445
Qy
661 CTTCTCTCAGCAGCGCTGGCCACCAAGTGCAGAGCAGCCACCACTGAGGAAGCGAG 720
Db
2446 CTTCTCTCAGCAGCGCTGGCCACCAAGTGCAGAGCAGCCACCACTGAGGAAGCGAG 2505
Qy
721 TGGCTGAGTGCAGTGGCGAGCTGAGGCGATGGCTTCTTCAAGAGCAGCCCTTTA 780
Db
2506 TGGCTGAGTGCAGTGGCGAGCTGAGGCGATGGCTTCTTCAAGAGCAGCCCTTTA 2565
Qy
781 AGGATTTCTGACAGCGCTTCTACGACAAAGTTTCTGAGTGGAACTCTTTCAGATGC 840
Db
2566 AGGATTTCTGACAGCGCTTCTACGACAAAGTTTCTGAGTGGAACTCTTTCAGATGC 2625
Qy
841 AACAGTGTACAGAGTACTTCACTGATTCAGAGTGTGGGAAAGTGTGTTTGGGG 900
Db
2626 AACAGTGTACAGAGTACTTCACTGATTCAGAGTGTGGGAAAGTGTGTTTGGGG 2685
Qy
901 AGGTATGTCCTGAGTGAAGAAACACTGCGGAAGTGTAT 941
Db
2686 AGGTATGTCCTGAGTGAAGAAACACTGCGGAAGTGTAT 2726

RESULT 11
US-08-464-954A-2
; Sequence 2, Application US/08464954A
; Patent No. 6255069
; GENERAL INFORMATION:
; APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,
; APPLICANT: PRIYA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR
; TITLE OF INVENTION: KINASES GRK5 AND GRK6
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESS: Jane Massey Licata, Esq.
STREET: Woodland Falls Corporate Park
STREET: 210 Lake Drive East, Suite 101
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,954A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076,084
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2848
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-464-954A-2

Query Match 19.1%; Score 419.8; DB 3; Length 2848;
Best Local Similarity 56.2%; Pred. No. 3.1e-97;
Matches 891; Conservative 0; Mismatches 682; Indels 12; Gaps 5;
Qy 305 GGCCTGCAGAACCTGATCGCCAAACAGCGCTACTGACAGCCCGGAGCCCTCGGACTG 364
Db 65 GGAGCTCGAAGAACATCGTAGCGAAGACAGCTGCTACTCAAGGCCCGGAGGTGGCGTGG 124
Qy 365 CGACAGCAAG-AGCTGCAGCGCGGCGGTAGCTGCGCCCTGCGCGGCTGCAGGG 421
Db 125 AAATCGCAAGCAAGCAAGAAATGCGCGCAGATGCTCCAGTTCCCTCATCAGCA 184
Qy 422 CTGCGGAGCTCGCCAGAAAGCTGCTCCGAACTTCCACAGCTGTGTGAGCAGCAGCC 481
Db 185 GTGCGAAGAGTGGCGGTGAGCTCGAGCGTGAATATCACAGCTGTGCGAGCGCAGC 244
Qy 482 CATCGTCCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTGCCTCCGCGGCGC 541
Db 245 CATTTGGCGCTGCTGTTCGAGAGTCTGTGCGAAGCGGCGGAGCTGAGCGCTGGCT 304
Qy 542 AACCTTCTAGAGCAGTGGGAACTGGGAGCTGGCGAGGAGGAGCCACCAAGAGCAG 601
Db 305 CGCTTCTGATGGGTGGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 364
Qy 602 CGCGCTGCGAGGGGTGGTGCGCACTTGTGCGAGTGCCTGCGCGCGGGAACCCGCAACC 661
Db 365 TGGCGGCGCAG- -TAAACGCAAGAAATTTCTGAGCCACACAGGCTCTGACCTCATCCTGA 421
Qy 662 CTTCTCAGCAGCGCGCTGGCCACCAAGTGCACAGCAGCCACCAAGAGAGCGAGT 721
Db 422 GGTCCCGCGCAGCTGGTGAGCAAC- -TGACCCCGGCTGAGCAGAGGTCTCCCTCAAG 480
Qy 722 GGCTGAGTGCAGCTGCGCAAGGCTGAGCCATGCTTTTTCGAGAGCAGCCCTTTAA 781
Db 481 ACCTTTCCAGGAAGTCAACCGGCTGA- -CCACGAGTACCTGAGCGTGGCGCTTTGC 538
Qy 782 GGATTTGCTGACCGCGCTTCTAGCAAGTCTTTCAGTGGAAACTCTTCAGATGCA 841

Db 539 CGAGTACCTCGACAGCATCTCTCAACCGTTTCTCGAGTGAAGTGGCTGGAAAGGCA 598
Qy 842 ACCAGTGTGACAGAGTACTTCACTGAGTTCAGAGTGTGGGGAAAGGTGGTGGGA 901
Db 599 GCAGGTGACAAAACACCTTTCAGGCAATACCGAGTCTCTGGGCAAGGTGGCTTTGGGA 658
Qy 902 GGTATGTGCGTCCAGGTGAAACACCTGGGAAGATGTATGCTGTAGAACTGGACAA 961
Db 659 GGTGTGCGCTCCAGGTGCGGGCCACAGGTAAAGTGTATGCTGTGAAGACTAGAGAA 718
Qy 962 GAAGCGGCTGAAGAAAGGTGGGAGAGATGGCTCTCTTGGAAAAGGAAATCTTGA 1021
Db 719 AAAGCGGATCAAGAGCGAAAGGGAGGCCATGGCGCTGAACGAGACAGATCTTGA 778
Qy 1022 GAAGTACAGACCCCTTTCATTTGTCTCTGCGCTATGCTTTGAGAGCAAGACCATCT 1081
Db 779 GAAAGTGAACAGTAGTGTGTAGTGAAGTGTGCTTACGCTATGAGCAACGAGCGCT 838
Qy 1082 CTGCTTGTGATGAGCTGATGAATGGGGAGACCTCAAGTTCACATCTACAACTGGG 1141
Db 839 GTGCTGTGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCACATCTACCAATGG 898
Qy 1142 CAGCGTGTGCGCTGAGCATGAGCGGGTGTATCTTTTACTCGGCCAGATAGCCTGTGGAT 1201
Db 899 CCAGGCTGGCTTCCCGAAGCGGGCGCTCTTCTACGCGCGAGATCTGTGTGGCT 958
Qy 1202 GGTGACCTTCATGAATCTGCGCATCGTCTATCGGACATGAAGCTGAGAAATGTCTTCT 1261
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Qy 1262 GGATGACCTGCGCACTGAGGTTTATCTGACCTGGGGTGGCGCTGGAGTGAAGGGTGG 1321
Db 1019 GGATGACCAAGCGGACATCGCATCTCTGACCTGGGACTAGCTGTGCTGCGCGAGG 1078
Qy 1322 CAAGGCCATCACCCAGAGGGCTGGAACCAATGTTTACATGCTGCTGAGATCCTAATGA 1381
Db 1079 CCAGACCATCAAGGGCGTGTGGGACCGTGGGTTACATGGCTCCGGAG---GTGGTGA 1135
Qy 1382 AAGTGAAGTTATCTCTCTGTGGACTGTTTGGCCATGGGATGAGCATTTATGAAT 1441
Db 1136 GAATGAACGGTACAGCTTCAGCGCTGACTGTGGGGCGCTCGGCTGCTCTGTACGAT 1195
Qy 1442 GTTGTCTGACGACACCATTCAGAGTTAAGGAAAGGTCAAGTAAAGAGGATCTGAA 1501
Db 1196 GATCAGCGCCAGTGCCTTCCAGCAGAGGAAGAGATCAAGCGGGAGGAGGTGA 1255
Qy 1502 GCAAGAACTCTGCAAGAGAGGTCAAAATCCAGCATGATTAATTCACAGAGGAACAA 1561
Db 1256 GCGGCTGTGAAGAGGTCCTCGAGAGTATTCGAGCGGTTTTCCCGAGCGCGCTC 1315
Qy 1562 AGATATTTGAGGCTCTTCTTGGCTAAGAAACAGAGCAACCTTTAGGAAGCAGAGAAA 1621
Db 1316 ACTTGTCTCACAGCTCTCTGCAAGGACCTTGCAGCGCTGGGGTGTGTGGGGCAG 1375
Qy 1622 GTCTGATATCCAGGAAACATCTTCTTTAAACGATCAACTTTCCTGCTGCTGGAAGC 1681
Db 1376 TGCCCGGAGGTGAAGAGGACCCCTCTTTAAGAAAGTGAATTTCAAGCGGCTGGAGC 1435
Qy 1682 TGGCTTAATGAACCCCATTTGTGCGAGACCTTTCAGTGGTTTATGCCAAGACATCGC 1741
Db 1436 TGGCATGTGGAGCGCGCTTCAAGCCTGACCCCGAGGCTTTTACTGCAAGGATGTCT 1495
Qy 1742 TGAATATGATTTTCTCTGAGGTTTCGGGGGTGGAATTTGATGACAAAGATAACAGTT 1801
Db 1496 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGAGCCCTACCGACAGCATT 1555
Qy 1802 CTTCAAAATTTGCGACAGGTGCTTCTTATAGCATGGCAGGAAGAAATTTATGAAC 1861
Db 1556 CTACCAGAAATTTGCGACAGGAGTGTGCCCATCCCTTCCGAGACGAGATGTTGGAGAC 1615
Qy 1862 GGGACTGTTTGGGAACTGAATGAC 1886
Db 1616 CGAGTGTTCGAAGAGCTGAATGTC 1640

RESULT 12

US-08-221-817-12
; Sequence 12, Application US/08221817
; Patent No. 5532151
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Merle F.
; TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,817
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532151and, Greta B.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
US-08-221-817-12

Query Match 19.0%; Score 418.2; DB 1; Length 2204;
Best Local Similarity 56.2%; Pred. No. 7.1e-97;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

Qy 305 GGCCCTGGACAACTGATCGCAACACCGCTACTCTGAGCGCCGGAAGCCCTCGGACTG 364
Db 33 GGAGCTCGAAGCAATCGTAGCGAACAACGCTGCTACTCAAGGCCCGGAGGTGGCGGTGG 92
Qy 365 CGACGACAAAG---AGCTGCAGCGCGCGGCGGTAGCCTTGGCCCTGCGGGCTGCAGGG 421
Db 93 AAATCGCAAGGCAAGAAATGGCGCAGATGCTCCAGTTTCCCTCACATCAGCA 152
Qy 422 CTGGCGGAGTCTCGCCGAGAGCTGTCCCTGAACTTCCACAGCTGTGTGAGCAGCACC 481
Db 153 GTGCGAAGAGTGGGGTTCAGCTCGAGCGTGAATATCACAGCTGTGCGAGCGGACCG 212
Qy 482 CATGGTGGCGGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTCCGAGGCGGC 541
Db 213 CATTGGGCGGCTGCTGTTCCGAGAGTCTGTGTCACAGGCGGAGCTGAGCCGCTGCGT 272

QY 542 AACCTTCTAGAGGACGTGCGAAGCTGGAGCTGGCCGAGGAGGACCCACCAAGACAG 601
Db 273 CGCCTTCTGGATGGGTGGCGAGTATGAAGTACCCCGGATCAAGCGGAGGCGATG 332
QY 602 CGCGCTGAGGGGCTGGTGGCACTTGTGCGAGTGCCTCGCCCGGGGAACCCGCAACC 661
Db 333 TGGCGGGGACG---TAACGCAAGATTTTCTGAGCCACACGCGGTCTGACCTCATCCCTGA 389
QY 662 CTTCTCTAGCAGCGCGTGGCCACCAAGTGCCACGAGCCACCACTGAGGAAGAGCGAGT 721
Db 390 GGTCCCCCGGACGTGGTGAAGAAC-TGACCCAGCGGTGAGGAGGAGGTCCCTGCAAG 448
QY 722 GCGTGCAGTGACGTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAGCAGCCCTTTAA 781
Db 449 ACCTTTTCCAGGAACCTACCCGGCTGA--CCACAGTAGCTGAGCGTGGCCCTTTTCG 506
QY 782 GGAATTTGAGCAGCGCTTCTAGCAAGTTTCTGCAAGTGGAACCTCTTCGAGATGCA 841
Db 507 CGAGTACCTCGACAGCATCTACTTCAACCGTTTCTGCAAGTGAAGTGGCTGGAAGGCA 566
QY 842 ACCAGTGTGACAGAGTACTTCACTGAGTTCAAGTGTGCGGAAAGTGGTTTTGGGGA 901
Db 567 GCAGTGACCAAAACACCTTCAGGCAATACCGAGTCTTGGTAAAGTGGCTTTGGGGA 626
QY 902 GGTATGTGCGCTCCAGGTGAACAAACACTGGGAAGATGTATGCTCTGAAGAACTGGACAA 961
Db 627 GGTGTGCGCTCCAGGTGCGGGCCACAGGTAAAGATGTATGCTCTGAAGAGCTAGAGAA 686
QY 962 GAAGCGGTGAAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAGGAAATCTTGA 1021
Db 687 AAAGCGGATCAAGAAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGA 746
QY 1022 GAAGGTGACAGCCCTTTTCATTGTCTCTGCGCTATGCTTTGAGAGCAAGACCACT 1081
Db 747 GAAAGTGAACATAGTTTGTAGTGAAGTGGCTTACCGCTATGAGCAAGAGCGCGCT 806
QY 1082 CTGCTTGTGATGAGCTGATGAATGGGGAGACCTCAAGTTTCCACATCTACAAGCTGGG 1141
Db 807 GTGCTGTGCTGACACTGATGAACGGGGCGACCTCAAGTTTCCACATCTACCACATGGG 866
QY 1142 CAGCGTGGCTGGACATGAGCGGGTGATCTTTTACTCGGCCAGATAGCTTGGGAT 1201
Db 867 CCAGGCTGGCTTTCCCGAAGCGCGGCGCTCTTCTACGCGCGGAGATCTGCTGGGCT 926
QY 1202 GCTGACCTCCATGAACCTCGGCATCGTCTATCGGACATGAAGCTGAGATGCTTCT 1261
Db 927 GAGGACCTGCACCGGAGCGCATCGTGTACGGGACCTGAAGCCCGAGAACATCTTCT 986
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Db 987 GATGACCAAGCCACATCCGATCTCTGACCTGGGACTAGCTGTGCAATGTGCCGAGGG 1046
QY 1322 CAGGCCATCACCCAGAGGCTGGAACCAATGGTTACATGGCTCTGAGATCTTAATGA 1381
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QY 1382 AAGGTAGTATTCTTCTCTGTGAGCTGGTTTCCCATGGATGACGATTTAGTAAAT 1441
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QY 1502 GCAAGAACTCTGCAAGAGAGGTCAATTCAGCATGATTAATCTTCAGAGAGAAACAAA 1561
Db 1224 GCGGCTGTGAAGAGGTCGCCGAGAGTATTCGAGGCGCTTTTCCCGCAGCGCCGCTC 1283
QY 1562 AGATATTGCGGCTCTTCTGGCTTAAGAAACAGAGCAACGCTTAGGAGCAGAGAAA 1621
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QY 1622 GTCTGATGATCCAGGAAACATCAATTTCTTTAAACGATCAACTTTCTCTCGCTGGAAGC 1681

Db 1344 TGCCCGGAGGTGAAGGAGCACCCCTCTTTAAAGAGCTGAACCTCAAGCGCTGGGAGC 1403
QY 1682 TGGCTTAATCAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCAAGACATCGC 1741
Db 1404 TGGCATGTGAGCGCGGCTTCAAGCCTTGACCCCGAGCCATTTACTCAAGGATGTTCT 1463
QY 1742 TGAATATGATATTTCTCTGAGGTTTCGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
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Db 1524 CTACAGAAGTTTGCCACAGGAGTGTGCCCATCCCTGGCAGAACGAGATGTTGGAGAC 1583
QY 1862 GGGACTGTTTGAGGAACCTGATGAC 1886
Db 1584 CGAGTGCTTCCAAGAGCTGAATGTC 1608

RESULT 13

US-08-454-439-12
; Sequence 12, Application US/08454439
; Patent No. 5591618
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Merle F.
; TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,439
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,817
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5591618and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
US-08-454-439-12


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RESULT 14
PCT-US94-10487-12
; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marehall, O'Toole, Geretein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10487
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,817
; FILING DATE: 31 MAR 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993

```

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/31981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2204 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 31..1758
 PCT-US94-10487-12

Query Match 19.0%; Score 418.2; DB 5; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 7.1e-97;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

305 GGCCTTGGACAACTGATCGCCCAACACCGCCTACCTGACAGGCCCGGAGCCCTCGGACTG 364
 Db 33 GGAGCTCGAGACATCGTAGCGNACACGGTGTCTCAAGGCCCGGAGGTGGCGTGG 92
 365 CGACAGCAAG---AGCTCGAGCGCGCGGTGAGCTGCGCCCTGCGCGGCTCGAGGG 421
 Db 93 AAATCGCAAGGCAAAAGCAAGAAATGGCGGAGATGCTCCAGTTCCCTCACATCAGCCA 152
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 Db 213 CATGGCGGCTGCTGTTCCGAGAGTTCGTGCGAGGCGCGAGCTGAGCGGTGCGT 272
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 602 CGCGTTCAGGGGCTGGTGGCCACTTGTGCGAGTGGCCCTGCGCGGGAACCCGCAACC 661
 Db 333 TGGCGGACG---TAACGCAAAATTTCTGAGCCACACGGTCTCGACCTCATCCCTGA 389
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 Db 449 ACCTTTTCCAGGAACCTACCCGGCTGA--CCACAGTACCTGAGCGTGGCGGCTTTTGC 506
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1022 GAAGGTGAGCAGCCCTTTTCATTTGTTCTCTCTGCGCTATGSCCTTTGAGACCAAGACCATCT 1081
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 Db 807 GTGCTGTGTCTGACACTGATGAACGGGGGAGCTCAAGTTTCCACATCTACCAACATGGG 866
 1142 CACGGTGGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCGAGATAGCTGTGGAT 1201
 Db 867 CCAGCTGGCTTCCCGAAGCGCGGGCGCTTCTTACGCCCGGAGATCTGCTGTGGCT 926
 1202 GCTGACCTCATGAACCTCGGCATCTCTATCGGGACATGAAGCTGAGATGCTTCT 1261
 Db 927 GGAGGACCTGACCGGGAGCGCATCTGTACAGGACCTGAAGCCCGGAGACATCTTCT 986
 1262 GGATGACCTCGGCAACTGACGTTTATCTGACCTGGGGCTGGCGGTGGAGATGAAGGGTGG 1321
 Db 987 GGATGACCCAGCGCACATCCGCACTCTCTGACCTGGGACTAGCTGTGATGTGCCGAGGG 1046
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 Db 1047 CCAGACCATCAAGGGCGGTGTGGGCACCGTGGGTATACATGGCTCCGAG---GTGGTGA 1103
 1382 AAAGTAAAGTTATTCTTATCTCTGAGCTGTTTCCATGGGATGCGAGCATTTATGAAT 1441
 Db 1104 GAATGAACGGTACAGTTTACGCTTACGCTTGGCGCTGCTGCTGCTGCTGACGAT 1163
 1442 GGTGTGAGGACGACACATTTCAAAGATTACAAGGAAAGGTCAAGTAAAGAGTCTGAA 1501
 Db 1164 GATCGAGGCGAGTGGCGCTTCCAGCAGAGAGGAAGAGATCAAGCGGAGGAGGTGA 1223
 1502 GCAAGAAACTCTGCAAGCAGGTCAATTTCCAGCATGATACTTTCACAGGAGGAGCAAA 1561
 Db 1224 CGGCTGGTGAAGAGGTCCCGAGGATATTCGAGCGCTTTTCCCGCAGGCCCGCTC 1283
 1562 AGATATTTGCAAGGCTCTTCTGGTAAAGAAACACAGAGCAAGCTTTAGGAACAGAGAAA 1621
 Db 1284 ACTTGTCTACAGTCTCTCTGCAAGGACCTTCCGAGCGCTGGGGTGTCTGTTGGGGCAG 1343
 1622 GTCTGATGATCCCAAGGAAACATCAATTTCTTAAACGATCAACTTCTCGCTTGGAGC 1681
 Db 1344 TGCCCGGAGGTGAAGGAGCACCCCTCTTTAAGAACTGAACCTTCAAGCGCTGGGAGC 1403
 1682 TGGCTTAATTGAACCCCACTTGTGCCAGACCTTCACTGGTGTATGCCAAGACATCGC 1741
 Db 1404 TGGCATCTGAGCGCGCGTTCAAGCCTGACCCCGGCGCATTTTCTGCAAGGATGTCT 1463
 1742 TGAATTTGATGATTTCTCTGAGGTTCCGGGGGTGGAAATTTGATGACAAAGATAAGCAGTT 1801
 Db 1464 GGACATTTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACGAGCTT 1523
 1802 CTTCAAAACTTTTGGCAGAGTGTCTTCTATAGCATGGCAGGAGAAATTTATAGAAAC 1861
 Db 1524 CTACAGAAGTTTGGCAGAGTGTGCCCATCCCTGGCAGAACGAGATGGTGGAGAC 1583
 1862 GGGACTGTTTGGAACTGAATGAC 1886
 Db 1584 CGAGTGTCTTCAAGAGCTGAATGTC 1608

RESULT 15
 US-08-221-817-21
 ; Sequence 21 Application US/08221817
 ; Patent No. 5532151
 ; GENERAL INFORMATION:
 ; APPLICANT: Chantry, David
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Hoeckstra, Merle F.
 ; TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
 ; TITLE OF INVENTION: Kinase GRK6
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:

```

; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSES: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,817
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 553215land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..1740
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US-08-221-817-21

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Query Match      18.0%; Score 395.8; DB 1; Length 1983;
Best Local Similarity 55.3%; Pred. No. 3.7e-91;
Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

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Job time : 374.848 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2005, 00:07:33 ; Search time 2882.42 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5652332 seqs, 3060109652 residues
Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2008.8	91.4	2249	9 US-09-802-117-5	Sequence 5, Appli
3	2008.8	91.4	2249	14 US-10-217-745-3	Sequence 5, Appli
4	1659	75.5	1659	13 US-10-044-205A-3	Sequence 3, Appli
5	1658.8	75.5	1662	17 US-10-311-034-45	Sequence 45, Appl
6	1658.8	75.5	1662	17 US-10-451-168-49	Sequence 49, Appl
7	1658.8	75.5	1662	19 US-10-788-197-22	Sequence 22, Appl
8	1658.4	75.5	1662	9 US-09-802-117-1	Sequence 1, Appli
9	1658.4	75.5	1662	14 US-10-217-745-1	Sequence 1, Appli
10	1657.2	75.4	1662	9 US-09-964-469-1	Sequence 1, Appli
11	1657.2	75.4	1662	16 US-10-425-962-1	Sequence 1, Appli

12	1640.8	74.6	1701	17 US-10-072-012-273	Sequence 273, App
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17	423	19.2	1683	19 US-10-788-197-8	Sequence 6, Appli
18	423	19.2	1770	19 US-10-788-197-6	Sequence 10, Appli
19	418.2	19.0	2848	19 US-10-788-197-10	Sequence 2, Appli
20	418.2	19.0	2848	10 US-09-851-686-2	Sequence 4, Appli
21	418.2	19.0	2848	10 US-09-873-367C-142	Sequence 142, App
22	418.2	19.0	2848	17 US-10-159-856-4	Sequence 24, Appl
23	418.2	19.0	2848	19 US-10-843-641A-142	Sequence 621, App
24	407.4	18.5	1692	19 US-10-788-197-24	Sequence 110, App
25	401.6	18.3	2817	17 US-10-388-934-621	Sequence 12, Appl
26	379.4	17.3	2467	15 US-10-084-817-110	Sequence 13, Appl
27	377.8	17.2	1773	19 US-10-788-197-12	Sequence 72, Appl
28	377.8	17.2	2519	13 US-10-071-766-13	Sequence 60, Appl
29	374.6	17.0	2519	10 US-09-971-392-72	Sequence 42, Appl
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40	320.6	14.6	1737	16 US-10-325-430-2	Sequence 16, Appl
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44	320.6	14.6	2113	19 US-10-677-983-7	Sequence 14, Appl
45	311.6	14.2	1503	19 US-10-788-197-14	

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; TITLE OF INVENTION: Uses
; FILE REFERENCE: 10147-5201
; CURRENT FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5

US-10-311-034-45
; Sequence 45, Application US/10311034
; Publication NO. US20040023242A1

; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYHER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeer

; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

Query Match 75.5%; Score 1658.8; DB 17; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGTGGACATGGGGGCCCTGGACAACTGATCGCCAAACACCGCTACCTGCAGGCCCGG 350
Db 1 ATGTGGACATGGGGGCCCTGGACAACTGATCGCCAAACACCGCTACCTGCAGGCCCGG 60
QY 351 AAGCCTCGGACTCGGACAGCAAGAGCTGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 410
Db 61 AAGCCTCGGACTCGGACAGCAAGAGCTGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120
QY 411 GGGCTGACAGGCTCGCGGGAGCTCCGCCAGAGCTGCTTCCCTGAACTTCCACAGCCTGTGT 470
Db 121 GGGCTGACAGGCTCGCGGGAGCTCCGCCAGAGCTGCTTCCCTGAACTTCCACAGCCTGTGT 180
QY 471 GAGCAGCAGCCCATCGGTCGCGGCTCTTCCGTGACTTCTTAGCAGCAGTGCACCGTTC 530
Db 181 GAGCAGCAGCCCATCGGTCGCGGCTCTTCCGTGACTTCTTAGCAGCAGTGCACCGTTC 240
QY 531 CGCAAGCGGGCAACCTTCTTAGAGGAGCTGAGAGCTGGGAGCTGGCGGAGGAGGAGCC 590
Db 241 CGCAAGCGGGCAACCTTCTTAGAGGAGCTGAGAGCTGGGAGCTGGCGGAGGAGGAGCC 300
QY 591 ACCAAGACAGCGGCTGCGAGGGCTGCGCCACTTGTGCGAGTGCCTTCCCGGGGG 650
Db 301 ACCAAGACAGCGGCTGCGAGGGCTGCGCCACTTGTGCGAGTGCCTTCCCGGGGG 360
QY 651 AACCCGCAACCTTCTTAGCAGCGGCTGGCCACCAAGTGCACAGCAGCCACCTGAG 710
Db 361 AACCCGCAACCTTCTTAGCAGCGGCTGGCCACCAAGTGCACAGCAGCCACCTGAG 420
QY 711 GAAGAGCGAGTGGCTGAGTGCAGTGCAGCGGCAAGGCTGAGGCCATGGCTTCTTTCAGAG 770
Db 421 GAAGAGCGAGTGGCTGAGTGCAGTGCAGCGGCAAGGCTGAGGCCATGGCTTCTTTCAGAG 480
QY 771 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTTACGACAAGTTTCTGCAAGTGAAGACTC 830
Db 481 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTTACGACAAGTTTCTGCAAGTGAAGACTC 540
QY 831 TTCAGATGCAACAGTGTGAGCAAGTACTTCACTGAGTTCAGAGTGTGGGAAAGGT 890
Db 541 TTCAGATGCAACAGTGTGAGCAAGTACTTCACTGAGTTCAGAGTGTGGGAAAGGT 600
QY 891 GGTTTTGGGAGGTTGTCGGCTCCAGGTGAAAAACACTGGGAGATGTATGCTGTAAAG 950
Db 601 GGTTTTGGGAGGTTGTCGGCTCCAGGTGAAAAACACTGGGAGATGTATGCTGTAAAG 660
QY 951 AAATGACAAAGAGCGGCTGAAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAG 1010
Db 661 AAATGACAAAGAGCGGCTGAAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAG 720
QY 1011 GAAATCTTGAGAAAGGTTCAGAGCCCTTTTCATTTGCTCTCTGCGCTATGCTTTGAGAGC 1070

Db 721 GAAATCTTGGAGAGGTGAGAGCCCTTTCATGTCTCTGGCCCTATGCTTGGAGC 780
Qy 1071 AAGACCCATCTGCTCTTGTATGAGCCTGATGAATGGGGAGAGCTCAAGTTTCCACATC 1130
Db 781 AAGACCCATCTGCTCTTGTATGAGCCTGATGAATGGGGAGAGCTCAAGTTTCCACATC 840
Qy 1131 TACAACTGGGACCGCGTGGCTGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 1190
Db 841 TACAACTGGGACCGCGTGGCTGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 900
Qy 1191 GCCTGTGGATGCTGACCTCATCACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
Db 901 GCCTGTGGATGCTGACCTCATCACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
Qy 1251 AATGTGCTTCTGGATGACCTCGGCAACTGCGAGTTTATCTGACCTGGGGCTGGCCGTGGAG 1310
Db 961 AATGTGCTTCTGGATGACCTCGGCAACTGCGAGTTTATCTGACCTGGGGCTGGCCGTGGAG 1020
Qy 1311 ATGAAGGTGGCAAGCCCATCAACCAGAGGGCTGGAACCAATGGTTTACATGGCTCTGAG 1370
Db 1021 ATGAAGGTGGCAAGCCCATCAACCAGAGGGCTGGAACCAATGGTTTACATGGCTCTGAG 1080
Qy 1371 ATCTTAATGGAAGGTAAAGTTATCTTCTATCTGAGCTGGTTTGGCCATGGGATGAGC 1430
Db 1081 ATCTTAATGGAAGGTAAAGTTATCTTCTATCTGAGCTGGTTTGGCCATGGGATGAGC 1140
Qy 1431 ATTTATGAAATGTTGCTGGAGCAACACATTTCAAGAGTTTCAAGGAAAGAGTCAAGTAA 1490
Db 1141 ATTTATGAAATGTTGCTGGAGCAACACATTTCAAGAGTTTCAAGGAAAGAGTCAAGTAA 1200
Qy 1491 GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGGTCAAAATTCAGCATGATACTTCA 1550
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCAGAGGTCAAAATTCAGCATGATACTTCA 1260
Qy 1551 GAGGAGCAAGAGATATTGCGAGCTCTTCTGGCTAAGAAACAGAGCAAGCTTAGGA 1610
Db 1261 GAGGAGCAAGAGATATTGCGAGCTCTTCTGGCTAAGAAACAGAGCAAGCTTAGGA 1320
Qy 1611 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCT 1670
Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCT 1380
Qy 1671 CGCTGGAAGCTGGCTAATTAAGACCCCATTTGTGCCAGACCTTCAGTGGTTTATGCC 1730
Db 1381 CGCTGGAAGCTGGCTAATTAAGACCCCATTTGTGCCAGACCTTCAGTGGTTTATGCC 1440
Qy 1731 AAAGACATCGTGAAATTTGATGATTTCTGAGGTTTGGGGGTGGAATTTGATGACAAA 1790
Db 1441 AAAGACATCGTGAAATTTGATGATTTCTGAGGTTTGGGGGTGGAATTTGATGACAAA 1500
Qy 1791 GATAGCAGTTTCTTCAAAACCTTTCGACAGTGTCTTCTATAGCATGGCAGGAAGAA 1850
Db 1501 GATAGCAGTTTCTTCAAAACCTTTCGACAGTGTCTTCTATAGCATGGCAGGAAGAA 1560
Qy 1851 ATTATAGAAACGGGACTGTTTGGAGAACTGATGACCCCAACAGACCTTACGGGTTGAG 1910
Db 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGATGACCCCAACAGACCTTACGGGTTGAG 1620
Qy 1911 GAGGTAATTCATCCAGTCTGGCGTGTGTTGTTTATTGTAA 1952
Db 1621 GAGGTAATTCATCCAGTCTGGCGTGTGTTGTTTATTGTAA 1662

RESULT 6

US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-49

Query Match 75.5%; Score 1658.8; DB 17; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 291 ATGTGGACATGGGGGCGCTCGACAACTGATCGCAACACCGCTACTCTGAGCCCGG 350
Db 1 ATGTGGACATGGGGGCGCTCGACAACTGATCGCAACACCGCTACTCTGAGCCCGG 60
Qy 351 AAGCCCTCGACTGCGACAGCAAGAGCTGAGCGGGCGGGCTAGCTGCGCCCTGCCC 410
Db 61 AAGCCCTCGACTGCGACAGCAAGAGCTGAGCGGGCGGGCTAGCTGCGCCCTGCCC 120
Qy 411 GGGCTGAGGGCTCGGGGAGCTCGCCAGAGCTGCTCCCTGACCTTCCACAGCCCTGT 470
Db 121 GGGCTGAGGGCTCGGGGAGCTCGCCAGAGCTGCTCCCTGACCTTCCACAGCCCTGT 180
Qy 471 GAGCAGAGCCCATCGTGGCGGCTCTTCCGCTGACTTCTAGCCACAGTGCACAGTTC 530
Db 181 GAGCAGAGCCCATCGTGGCGGCTCTTCCGCTGACTTCTAGCCACAGTGCACAGTTC 240
Qy 531 CGCAAGCGGCAACCTTCTTAGAGGACGTGAGAACTGGGAGCTGGCGAGGAGGAGCC 590
Db 241 CGCAAGCGGCAACCTTCTTAGAGGACGTGAGAACTGGGAGCTGGCGAGGAGGAGCC 300
Qy 591 ACCAAGACAGCGCTGCGAGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCCGGG 650
Db 301 ACCAAGACAGCGCTGCGAGGGCTGGTGGCCACTTGTGGAGTGGCCCTGCCCCGGG 360
Qy 651 AACCGCAACCTTCTTCTCAGCAGCGCTGGCCACCAAGTGCAGAGCAGCCACTGAG 710
Db 361 AACCGCAACCTTCTTCTCAGCAGCGCTGGCCACCAAGTGCAGAGCAGCCACTGAG 420
Qy 711 GAAGAGCGAGTGGCTGACGTGACCGCTGCGCAAGGCTGAGGCAATGGCTTTCTTGAAGAG 770
Db 421 GAAGAGCGAGTGGCTGACGTGACCGCTGCGCAAGGCTGAGGCAATGGCTTTCTTGAAGAG 480
Qy 771 CAGCCCTTAAAGGATTTGTCAGCCAGCCCTTCTACGACAAAGTTCTTCAGTGGAACTC 830
Db 481 CAGCCCTTAAAGGATTTGTCAGCCAGCCCTTCTACGACAAAGTTCTTCAGTGGAACTC 540
Qy 831 TTCGAGATGCAACAGTGTGACAGAACTTCTACTGAGTTTCTAGAGTCTCGGGAAAGGT 890
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Qy	891	GGTTTTGGGAGGATATGTCGCGTCCAGGTGAAAAACACTGGGAAGATGTATGCTCTGTAAG	950
Db	601	GGTTTTGGGAGGATATGTCGCGTCCAGGTGAAAAACACTGGGAAGATGTATGCTCTGTAAG	660
Qy	951	AAACTGGACAAGACGGCTCAAGAAGAAAGTGGCGAGAGAAGTGGCTCTCTTTGGAAAG	1010
Db	661	AAACTGGACAAGACGGCTCAAGAAGAAAGTGGCGAGAGAAGTGGCTCTCTTTGGAAAG	720
Qy	1011	GAATCTTTGGAGAGGTCAGCAGCCCTTTTCATTGTCTCTCTGGCCTATGCTTTGAGAGC	1070
Db	721	GAATCTTTGGAGAGGTCAGCAGCCCTTTTCATTGTCTCTCTGGCCTATGCTTTGAGAGC	780
Qy	1071	AAGACCCATCTCTGCCCTGTTCATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC	1130
Db	781	AAGACCCATCTCTGCCCTGTTCATGAGCCTGATGAATGGGGAGACCTCAAGTTCACATC	840
Qy	1131	TACAACTGGCAGCGCTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA	1190
Db	841	TACAACTGGCAGCGCTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA	900
Qy	1191	GCCTGTGGGATGCTGCACCTCCATGAACCTGGCANCTGTCTATCGGGAATGAAGCCTGAG	1250
Db	901	GCCTGTGGGATGCTGCACCTCCATGAACCTGGCANCTGTCTATCGGGAATGAAGCCTGAG	960
Qy	1251	AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG	1310
Db	961	AATGTGCTTCTGGATGACCTCGGCNACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG	1020
Qy	1311	ATGAAGGGTGGCAAGCCCATCACCCAGGGCTGGAAACCAATGGTTACATGGCTCCTGAG	1370
Db	1021	ATGAAGGGTGGCAAGCCCATCACCCAGGGCTGGAAACCAATGGTTACATGGCTCCTGAG	1080
Qy	1371	ATCCTAATGGAAGGTTAAGTTATTCCTATCCTGTGGACTGGTTGGCATGGGATGGCAGC	1430
Db	1081	ATCCTAATGGAAGGTTAAGTTATTCCTATCCTGTGGACTGGTTGGCATGGGATGGCAGC	1140
Qy	1431	ATTTATGAAATGGTGTGTCGACGAACACCACTTCAAAGATTACAAGGAAAAAGGTCAGTAA	1490
Db	1141	ATTTATGAAATGGTGTGTCGACGAACACCACTTCAAAGATTACAAGGAAAAAGGTCAGTAA	1200
Qy	1491	GAGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCANATGATACTTCACA	1550
Db	1201	GAGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCAGCANATGATACTTCACA	1260
Qy	1551	GAGGAACAAAGATATTTGCAGGCTCTCTTGGCTAAGAAAACAGAGCAACGCTTAGGA	1610
Db	1261	GAGGAACAAAGATATTTGCAGGCTCTCTTGGCTAAGAAAACAGAGCAACGCTTAGGA	1320
Qy	1611	AGCAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTTAAAAACGATCAACTTTCCT	1670
Db	1321	AGCAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTTAAAAACGATCAACTTTCCT	1380
Qy	1671	CGCCTGAAGCTGGCCTTAATTGAACCCCAATTTGTGCCAGACCCCTTCAGTGGTTATGCC	1730
Db	1381	CGCCTGAAGCTGGCCTTAATTGAACCCCAATTTGTGCCAGACCCCTTCAGTGGTTATGCC	1440
Qy	1731	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAAATTCATGACAAA	1790
Db	1441	AAAGACATCGCTGAAATTTGATGATTTCTCTGAGGTTTCGGGGGTGGAAATTCATGACAAA	1500
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Db	1501	GATAAGCAGTCTTCAAACACTTTGGCAGAGGTGCTGTTCCTATAGCATGGCAGGAAGAA	1560
Qy	1851	ATTATAGAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACTCAGGGTCTGAG	1910
Db	1561	ATTATAGAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACTCAGGGTCTGAG	1620
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Db	1621	GAGGGTAATTCATCCAAAGCTGGCGGTGTTGTTATGTAA	1662

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RESULT 7
US-10-788-197-22
; Sequence 22, Application US/10788197
; Publication No. US20050032125A1
; GENERAL INFORMATION:
; APPLICANT: OAKLEY, ROBERT H.
; APPLICANT: HUDSON, CHRISTINE C.
; TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
; FILE REFERENCE: NRK.108
; CURRENT APPLICATION NUMBER: US/10/788,197
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/14561
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,986
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/401,698
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-197-22

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Query Match	75.5%; Score 1658.8; DB 19; Length 1662;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1660; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy	291 ATGTGTGACATGGGGGCCCTGGACAACCTGATCGCCAAACCGGCTACCTGCGAGGCCCGG 350
Db	1 ATGGTGGACATGGGGGCCCTGGACAACTGATCGCCAAACCGGCTACCTGCGAGGCCCGG 60
Qy	351 AAGCCCTCGACATGCGACAGACAAAGAGCTGCAGCGCGGGGGGTAGCTGGCCCTGCC 410
Db	61 AAGCCCTCGAGATCGGACAGACAAAGAGCTGCAGCGCGGGGGGTAGCTGGCCCTGCC 120
Qy	411 GGGCTGCAGGGCTGCGCGGAGGCTCCGCCAGAGCTGTCCTGAACTTCCACAGCGCTGTG 470
Db	121 GGGCTGCAGGGCTGCGCGGAGGCTCCGCCAGAGCTGTCCTGAACTTCCACAGCGCTGTG 180
Qy	471 GAGCAGAGCCCATCGGTGCGCGGCTTTCCGTGACTTCTTAGCCACAGTGCACACGTTTC 530
Db	181 GAGCAGCAGGCCATCGGTGCGCGGCTTTCCGTGACTTCTTAGCCACAGTGCACACGTTTC 240
Qy	531 CGCAAGCGGCAACCTTCTTAGAGGAGCTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
Db	241 CGCAAGCGGCAACCTTCTTAGAGGAGCTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
Qy	591 ACCAAAGACAGCGCTGCAGGGGCTGGTGGCCACATTTGCGAGTGCCTTCGCCCGGGG 650
Db	301 ACCAAAGACAGCGCTGCAGGGGCTGGTGGCCACTTTGTCGAGTGCCTTCGCCCGGGG 360
Qy	651 AACCCGCAACCTTCTCAGCAGAGCGGTGGCCACCAAGTGCCAGCAGCCACCACTGAG 710
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Qy	711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAG 770
Db	421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAAGGCTGAGGCCATGGCTTTCTTGAAGAG 480
Qy	771 CAGCCCTTTAAGATTTCTGTGACAGCGCCTTCTTAGCAAGTTTCTGCAGTGGAAATC 830
Db	481 CAGCCCTTTAAGATTTCTGTGACAGCGCCTTCTTAGCAAGTTTCTGCAGTGGAAATC 540
Qy	831 TTCGAGATGCAACAGTGTGACAGCAAGTACTTCCTAGTTTCAGAGTGTCTGGGGAAGGT 890
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Qy	891 GGTTTTGGGAGTATGTGCCCGTCCAGGTGAAAAACA CTGGGAAGATGTATGCTGTGAAG 950
Db	601 GGTTTTGGGAGTATGTGCGTCCAGGTGAAAAACA CTGGGAAGATGTATGCTGTGAAG 660

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Qy 951 AAATGGGCAAGAGCGGCTGAAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAAG 1010
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Qy 661 AAATGGGCAAGAGCGGCTGAAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAAG 720
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Qy 1011 GAAATCTTTGGAGAGGTGAGAGCGGCTTTCAATGTCTCTCTGGCTATGCTTGGAGAGC 1070
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Qy 721 GAAATCTTTGGAGAGGTGAGAGCGGCTTTCAATGTCTCTCTGGCTATGCTTGGAGAGC 780
Db |||||
Qy 1071 AAGACCCATCTCTGCTTTGTGATGAGCTGATGAATGGGGGAGAGCTCAAGTTTCACATC 1130
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Qy 1131 TACAAGCTGGGCAAGCGTGGCTGGACATGAGCGGGTGATCTTTACTCGGCCAGATA 1190
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Qy 841 TACAAGCTGGGCAAGCGTGGCTGGACATGAGCGGGTGATCTTTACTCGGCCAGATA 900
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Qy 1191 GCCTGTGGAGTGTGACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG 1250
Db |||||
Qy 901 GCCTGTGGAGTGTGACCTCCATGAACCTCGGCATCGTCTATCGGGACATGAAGCTGAG 960
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Qy 1251 AATGTGCTTTCTGGATGACCTCGGCAACTGCAAGTTTATCTGACCTGGGCTGGCGTGGAG 1310
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Qy 961 AATGTGCTTTCTGGATGACCTCGGCAACTGCAAGTTTATCTGACCTGGGCTGGCGTGGAG 1020
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Qy 1311 ATGAAGGTGGCAAGCGGCTGATGAGAGGCTGGAACCAATGTTTATGCTGCTGAG 1370
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Qy 1021 ATGAAGGTGGCAAGCGGCTGATGAGAGGCTGGAACCAATGTTTATGCTGCTGAG 1080
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Qy 1371 ATCTTAATGGAAGGTGAAGTTATCTCTGCTGAGTCTGTTGCTGCTGAGTGGAGTGGAGC 1430
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Qy 1081 ATCTTAATGGAAGGTGAAGTTATCTCTGCTGAGTCTGTTGCTGCTGAGTGGAGTGGAGC 1140
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Qy 1431 ATTTATGAAATGGTTGCTGGAAGCAACCAATTCAGAGATTACAGGAAAGGTGAGTAAA 1490
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Qy 1141 ATTTATGAAATGGTTGCTGGAAGCAACCAATTCAGAGATTACAGGAAAGGTGAGTAAA 1200
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Qy 1491 GAGGATCTGAAGCAAGAACTCTGCAAGACAGAGTCAAATTCAGAGTAACTTACAA 1550
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Qy 1261 GAGGACGAAAGATATTTGAGGCTCTCTGCTGAGTAAAGAACGAGCAAGCTTAGGA 1320
Db |||||
Qy 1611 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCT 1670
Db |||||
Qy 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCT 1380
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Qy 1671 CGCTGGAAGCTGGCTTAATTAACCCCATTTGTGCGAGACCCCTTCAGTGGTTATGCC 1730
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Qy 1851 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGAG 1910
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Qy 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGAG 1620
Db |||||
Qy 1911 GAGGTAATTCATCAAGTCTGGGCTGTTGTTGTTATTTGTA 1952
Db |||||
Qy 1621 GAGGTAATTCATCAAGTCTGGGCTGTTGTTGTTATTTGTA 1662
Db |||||
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RESULT 8

US-09-802-117-1

; Sequence 1, Application US/09802117

; Publication No. US20020042503A1

; GENERAL INFORMATION:

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; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polym
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-802-117-1
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Query Match 75.5%; Score 1658.4; DB 9; Length 1662;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 291 ATGCTGACATGGGGGCGCTGGACAACTGATCGCCACACCGCTACCTGCAGGCCGG 350
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Qy 1 ATGCTGACATGGGGGCGCTGGAYAACCTGATCGCCAAACCCGCTACCTGCAGGCCGG 60
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Qy 351 AAGCCCTCGACTCGGACAGCAAGAGCTGCAGCGGGCGGCTAGCTGGCCCTGCC 410
Db |||||
Qy 61 AAGCCCTCGGACTCGGACAGCAAGAGCTGCAGCGGGCGGCTAGCTGGCCCTGCC 120
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Qy 411 GGGCTGACGGCTCGCGGAGCTCCGCGAGAGCTGCTCCCTGAACTTCCACAGCTGTGT 470
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Qy 121 GGGCTGACGGCTCGCGGAGCTCCGCGAGAGCTGCTCCCTGAACTTCCACAGCTGTGT 180
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Qy 471 GAGCAGACGCCATCGGTGCGCCGCTCTTCGTGACTCTTAGCCACAGTGCACAGTTC 530
Db |||||
Qy 181 GAGCAGACGCCATCGGTGCGCCGCTCTTCGTGACTCTTAGCCACAGTGCACAGTTC 240
Db |||||
Qy 531 CGCAAGCGGCAACCTTTCTAGAGAGCTGCAGAACTGGGAGCTGGCGAGGAGGACCC 590
Db |||||
Qy 241 CGCAAGCGGCAACCTTTCTAGAGAGCTGCAGAACTGGGAGCTGGCGAGGAGGACCC 300
Db |||||
Qy 591 ACCAAGACAGCGGCTGCGAGGGCTGGTGCCCACTTTGTGCGAGTGGCCCTGCCCGGG 650
Db |||||
Qy 301 ACCAAGACAGCGGCTGCGAGGGCTGGTGCCCACTTTGTGCGAGTGGCCCTGCCCGGG 360
Db |||||
Qy 651 AACCCGCAACCTTTCTAGCAGCGGCTGGCCACCAAGTCCCAAGCGCCACCACTGAG 710
Db |||||
Qy 361 AACCCGCAACCTTTCTAGCAGCGGCTGGCCACCAAGTCCCAAGCGCCACCACTGAG 420
Db |||||
Qy 711 GAAGAGCGAGTGGCTGCACTGAGCTGCGCAAGGCTGAGGCACTGCTTCTTGAAGAG 770
Db |||||
Qy 421 GAAGAGCGAGTGGCTGCACTGAGCTGCGCAAGGCTGAGGCACTGCTTCTTGAAGAG 480
Db |||||
Qy 771 CAGCCCTTTAAGGATTTCTGACACAGCGCTTTACGACAAAGTTTCTGAGTGAACATC 830
Db |||||
Qy 481 CAGCCCTTTAAGGATTTCTGACACAGCGCTTTACGACAAAGTTTCTGAGTGAACATC 540
Db |||||
Qy 831 TTCAGATGCAACAGTGTGCAAGTACTTTCACTGAGTTTCAAGTGTCTGGGGAAGGT 890
Db |||||
Qy 541 TTCAGATGCAACAGTGTGCAAGTACTTTCACTGAGTTTCAAGTGTCTGGGGAAGGT 600
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Qy 891 GTTTTGGGAGGTATGTCGCTCCAGTGAAGAACTGGAAGAGATGATGCTGTGAAG 950
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Qy 951 AAATGGACAAAGAGCGGCTGAAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAAG 1010
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Qy 661 AAATGGACAAAGAGCGGCTGAAGAGAAAGGTGGCGAGAGATGGCTCTCTTGGAAAAG 720
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QY 1131 TACAACGTGGGACGCGTGGCTGGACATGAGCCGGTGATCTTTTACTCGGCCCCAGATA 1190
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QY 1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATGCTATGCGGACATGAAGCTGAG 1250
Db |||||
QY 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATGCTATGCGGACATGAAGCTGAG 960
Db |||||
QY 1251 AATGTGCTTCTGGATGACCTCGGCAACTCGAGGTTATCTGACTGGGGCTGGCCGTGGAG 1310
Db |||||
QY 961 AATGTGCTTCTGGATGACCTCGGCAACTCGAGGTTATCTGACTGGGGCTGGCCGTGGAG 1020
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QY 1311 ATGAAGGGTGGCAAGCCCATCAACCCAGAGGGCTGGAACCAATGGTTACATGCTCTGTAG 1370
Db |||||
QY 1021 ATGAAGGGTGGCAAGCCCATCAACCCAGAGGGCTGGAACCAATGGTTACATGCTCTGTAG 1080
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QY 1371 ATCCCTAATGGAAAGGTAAAGTTATTCCTATCTGTGGACTGGTTGCCATGGGATGCAGC 1430
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QY 1081 ATCCCTAATGGAAAGGTAAAGTTATTCCTATCTGTGGACTGGTTGCCATGGGATGCAGC 1140
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QY 1431 ATTATGAATGGTGTGCTGGACGAACACCAATCAAGAGATTACAAGGAAGGTCAAGTAA 1490
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QY 1141 ATTATGAATGGTGTGCTGGACGAACCAATCAAGAGATTACAAGGAAGGTCAAGTAA 1200
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QY 1551 GAGGAAGCAAGAGATATTGTCAGGCTCTCTGGCTTAAGAAACCGAGCAAGCTTAGGA 1610
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QY 1321 AGCAGAGAAAGCTCTGATGATCCAGGAAACATCAATCTTTTAAACAGTCAACTTCT 1380
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QY 1671 CGCTGGAGCTGGCTTAATGAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1730
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QY 1381 CGCTGGAGCTGGCTTAATGAACCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1440
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QY 1731 AAGACATCGCTGAATGATGATTTCTGAGGTTGGGGGTGGAAATTTGATGACAAA 1790
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QY 1441 AAGACATCGCTGAATGATGATTTCTGAGGTTGGGGGTGGAAATTTGATGACAAA 1500
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QY 1791 GATAAGCAGTTCTTCAAAAACCTTCGACAGGTGCTGTTCTATAGCATGGCAGGAAGA 1850
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Db |||||
QY 1851 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
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QY 1561 ATTATAGAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
Db |||||
QY 1911 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTGTTATGTAA 1952
Db |||||
QY 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTGTTATGTAA 1662
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RESULT 10

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US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
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; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1

Query Match      75.4%; Score 1657.2; DB 9; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 ATGTGGGACATGGGGGCCCTGGACAACTGATCGCCAAACACCGCTTACTGACGCCCCGG 350
Db |||||
QY 351 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGCGGTAGCTTGGCCCTGCC 410
Db |||||
QY 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGCGCGCGGTAGCTTGGCCCTGCC 120
Db |||||
QY 411 GGGCTGCAAGGGCTGCGCGAGCTCGCCAGAAAGCTGCTCCCTGAACTTCCACAGCTGTGT 470
Db |||||
QY 121 GGGCTGCAAGGGCTGCGCGAGCTCGCCAGAAAGCTGCTCCCTGAACTTCCACAGCTGTGT 180
Db |||||
QY 471 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCCTGCTTC 530
Db |||||
QY 181 GAGCAGCAGCCCATCGGTGCGCGCTCTTCCGTGACTTCTTAGCCACAGTGCCTGCTTC 240
Db |||||
QY 531 CGCAAGCGGCAACCTTCTTAGAGACCTGCGCAAGAACTGGGAGCTGGCGAGGAGGACCC 590
Db |||||
QY 241 CGCAAGCGGCAACCTTCTTAGAGACCTGCGCAAGAACTGGGAGCTGGCGAGGAGGACCC 300
Db |||||
QY 591 ACCAAGACAGCGCGCTCGAGGGCTGTGGCCACTTGTGCGAGTGCCTCGCCCGGG 650
Db |||||
QY 301 ACCAAGACAGCGCGCTCGAGGGCTGTGGCCACTTGTGCGAGTGCCTCGCCCGGG 360
Db |||||
QY 651 AACCGCAACCTTCTTAGAGCCCGCTGGCCACCAAGTGCACAGCAGCCACCTGAG 710
Db |||||
QY 361 AACCGCAACCTTCTTAGAGCCCGCTGGCCACCAAGTGCACAGCAGCCACCTGAG 420
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QY 711 GAAGAGCAGTGGCTGAGTGCAGCGTGGCAAGGCTGAGGCCATGGCTTCTTTCGAGAG 770
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QY 421 GAAGAGCAGTGGCTGAGTGCAGCGTGGCAAGGCTGAGGCCATGGCTTCTTTCGAGAG 480
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QY 771 CAGCCCTTTAAGGATTTCTGACACAGCGCTTCTACGACAACTTCTGCAAGTGAACATC 830
Db |||||
QY 481 CAGCCCTTTAAGGATTTCTGACACAGCGCTTCTACGACAACTTCTGCAAGTGAACATC 540
Db |||||
QY 831 TTGAGATGCAACCAAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTGTGCGGGAAGGT 890
Db |||||
QY 541 TTGAGATGCAACCAAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTGTGCGGGAAGGT 600
Db |||||
QY 891 GGTTTTGGGAGGTTATGTCGCTCAGGTGAAAAACACTGGGAAAGATGATGCTGTAAG 950
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QY 1011 GAAATCTTGGAGAAAGGTGAGCAGCGCTTTCATTGTTCTCTGCGCTATGCTTTCGAGAGC 1070
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QY 721 GAAATCTTGGAGAAAGGTGAGCAGCGCTTTCATTGTTCTCTGCGCTATGCTTTCGAGAGC 780
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QY 1071 AAGACCCATCTCTGCTTGTGATGAGCTGATGAATGGGGAGAGCTCAAGTTCCACATC 1130
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QY 781 AAGACCCATCTCTGCTTGTGATGAGCTGATGAATGGGGAGAGCTCAAGTTCCACATC 840
Db |||||
QY 1131 TACAAGTGGGACGCGCTGGCTGACATGAGCGGGTGATCTTTTACTCGGCCCCAGATA 1190
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QY 1251 AATGCTCTTCTGATGACCTCGGCAACTGACAGTTATCTGACCTGGGGCTGCGCGTGGAG 1310
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QY 961 AATGCTCTTCTGATGACCTCGGCAACTGACAGTTATCTGACCTGGGGCTGCGCGTGGAG 1020
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QY 1311 ATGAGGTTGGCAAGCCCATCCAGAGGGCTGGACCAATGGTTACATGGCTCTGAG 1370
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QY 1021 ATGAGGGTGGCAAGCCCATCCAGAGGGCTGGACCAATGGTTACATGGCTCTGAG 1080
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Db |||||
QY 1081 ATCTAAATGGAAGTAAAGTTATCTCTATCTGTTGAGCTGGTTTGGCCATGGATGCAGC 1140
Db |||||
QY 1431 ATTTATGAAATGGTTGCTGGAGCAACACCATTTCAAAGATTACAGGAAAAGTTCAGTAA 1490
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QY 1141 ATTTATGAAATGGTTGCTGGAGCAACACCATTTCAAAGATTACAGGAAAAGTTCAGTAA 1200
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QY 1491 GAGGATCTGAGCAAGAAAGTCTGCAAGACGAGTCAATTTCCAGCATGATCACTTCACA 1550
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QY 1201 GAGGATCTGAGCAAGAAAGTCTGCAAGACGAGTCAATTTCCAGCATGATCACTTCACA 1260
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QY 1551 GAGGAAGCAAGATATTTGAGGCTCTTCTGGCTTAAGAAACAGAGCAAGCTTAGGA 1610
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QY 1261 GAGGAAGCAAGATATTTGAGGCTCTTCTGGCTTAAGAAACAGAGCAAGCTTAGGA 1320
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QY 1611 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCT 1670
Db |||||
QY 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCT 1380
Db |||||
QY 1671 CGCTGGAGCTGGCTAAATTAACCCCATTTGTCAGACCTTCACTGTTTATGCC 1730
Db |||||
QY 1381 CGCTGGAGCTGGCTAAATTAACCCCATTTGTCAGACCTTCACTGTTTATGCC 1440
Db |||||
QY 1731 AAGACATCGCTGAATGATGATTTCTGAGGTTTGGGGGTGGAATTTGATGACAAA 1790
Db |||||
QY 1441 AAGACATCGCTGAATGATGATTTCTGAGGTTTGGGGGTGGAATTTGATGACAAA 1500
Db |||||
QY 1791 GATAAGCAGTTCTTCAAAACATTTTCGACAGGTGCTGTTCTTATAGCATGGCAGGAAGA 1850
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QY 1501 GATAAGCAGTTCTTCAAAACATTTTCGACAGGTGCTGTTCTTATAGCATGGCAGGAAGA 1560
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QY 1851 ATTATAGAAACGGGACTGTTGAGAACTGAATGATGACCCCAAGACCTTACGGGTTGTGAG 1910
Db |||||
QY 1561 ATTATAGAAACGGGACTGTTGAGAACTGAATGATGACCCCAAGACCTTACGGGTTGTGAG 1620
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QY 1911 GAGGTAATTCATCAAGTCTGCGCTGTTGTTGTTATTGTAA 1952
Db |||||
QY 1621 GAGGTAATTCATCAAGTCTGCGCTGTTGTTGTTATTGTAA 1662
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RESULT 12

US-10-072-012-273
; Sequence 273, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pens, Carol E. A
; APPLICANT: Furtak, Katarzyna

; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-273

Query Match 74.6%; Score 1640.8; DB 17; Length 1701;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1693; Conservative 0; Mismatches 2; Indels 21; Gaps 3;
QY 273 TGCGCCCGTCTCAGCCATGTTGGACATGGGGCCCTTGGACCACTGATGCCCAACACC 332
Db 1 TGCGCCCGTCTCAGCCATGTTGGACATGGGGCCCTTGGACCACTGATGCCCAACACC 60
QY 333 GCCTACTGCGAGGCCCGGAAGCCCTCGACATGGCAGACAGAAAGAGCTGCAGCGCGCGG 392
Db 61 GCCTACTGCGAGGCCCGGAAGCCCTCGACATGGCAGACAGAAAGAGCTGCAGCGCGCGG 120
QY 393 CGTAGCCTGGCCCTGCGCGGCTGCGCGAGCTCCGCCAGAGCTGTCCTCTG 452
Db 121 CGTAGCCTGGCCCTGCGCGGCTGCGCGAGCTCCGCCAGAGCTGTCCTCTG 180
QY 453 AACTTCCACAGCCTGTGTGACGACGAGCCCATCGGTGCGCGCTTCCGTGACTTCTTA 512
Db 181 AACTTCCACAGCCTGTGTGACGACGAGCCCATCGGTGCGCGCTTCCGTGACTTCTTA 240
QY 513 GCCACAGTGCCTCCGTCGCAAGCGGCAACCTTCTTAGAGGAGCTGCAGNACTGGGAG 572
Db 241 GCCACAGTGCCTCCGTCGCAAGCGGCAACCTTCTTAGAGGAGCTGCAGNACTGGGAG 300
QY 573 CTGGCCGAGGAGGAGACCCACCAAGACAGCGCTGCGAGGGGCTGCTGGCCACTTGTGG 632
Db 301 CTGGCCGAGGAGGAGACCCACCAAGACAGCGCTGCGAGGGGCTGCTGGCCACTTGTGG 360
QY 633 AGTGGCCCTGCGCGGGGAACCCGCAACCTTCTTAGCCAGCGCGCTGGCCCAAGTGC 692
Db 361 AGTGGCCCTGCGCGGGGAACCCGCAACCTTCTTAGCCAGCGCGCTGGCCCAAGTGC 420
QY 693 CAAGCAGCCACCTCTGAGGAAGAGGAGTGGCTGACGTGACGCTGCCGCAAGGCTGAGGCC 752
Db 421 CAAGCAGCCACCTCTGAGGAAGAGGAGTGGCTGACGTGACGCTGCCGCAAGGCTGAGGCC 480

QY 753 ATGCTTTCTTCAAGACGACCCCTTTAAGGATTTCTGACACGCGCTTCTTACGACAAG 812
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QY 481 ATGCTTTCTTCAAGACGACCCCTTTAAGGATTTCTGACACGCGCTTCTTACGACAAG 540
Db |||||
QY 813 TTTCTGAGTGGAAACTCTTTCGAGATGCAACACGAGTGTACAGCAAGTACTTCACTGAGTTC 872
Db |||||
QY 541 TTTCTGAGTGGAAACTCTTTCGAGATGCAACACGAGTGTACAGCAAGTACTTCACTGAGTTC 600
Db |||||
QY 873 AGAGTGTCTGGGAAAGAGTGTGTTGGGAGGTATGCGCGTCCAGGTGAAAAACACTGGG 932
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Db |||||
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QY 646 AAGATGTATGCTGTATGAAGAACTGGACAAGAGCGGCTGAAGAAAGAGTGGCGAGAAG 705
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QY 993 ATGGCTCTCTTGGAAAGGAAATCTTGGAGAGGTGAGAGCGCCCTTTCATTTGCTCTCTG 1052
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QY 706 ATGGCTCTCTTGGAAAGGAAATCTTGGAGAGGTGAGAGCGCCCTTTCATTTGCTCTCTG 765
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QY 1126 TGGTTTGCATGGATGACGATTTATGAAATGGTTTCTGGACGAAACACCATTCAAAGAT 1185
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QY 1470 TACAGGAAAGGTGATGAAGAGATCTGAAGCAAGAACTCTCTGCAAGAGAGTCAAA 1529
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QY 1186 TACAGGAAAGGTGATGAAGAGATCTGAAGCAAGAACTCTCTGCAAGAGAGTCAAA 1245
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QY 1306 AAACAGAGCAACGCTTAGGAGAGAGAGAGAGAGTCTGATGATCCAGAGAAACATCAT 1365
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QY 1647 TTCTTTAAACCATCAACTTCTGCTGAGAGTGGAGTGGCTTAATTTGAACCCCATTTGTG 1706
Db |||||
QY 1366 TTCTTTAAACCATCAACTTCTGCTGAGAGTGGAGTGGCTTAATTTGAACCCCATTTGTG 1425
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QY 1707 CCAGACCCCTTCAAGTGGTTTATGCCAAAGACATCGCTGAAATTTGATGATTTCTCTGAGTT 1766
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QY 1426 CCAGACCCCTTCAAGTGGTTTATGCCAAAGACATCGCTGAAATTTGATGATTTCTCTGAGTT 1485
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QY 1767 CGGGGGGTGAATTTGATGACAAAGATGAAGAGTTCCTTCAAAAACCTTTGCAAGGTGCT 1826
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QY 1486 CGGGGGGTGAATTTGATGACAAAGATGAAGAGTTCCTTCAAAAACCTTTGCAAGGTGCT 1545
Db |||||

QY 1827 GTTCTATAGCATGCGACGAGAAATATTAGAAACGGGACTGTTTGAGGAACTGAATGAC 1886
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QY 1546 GTTCTATAGCATGCGACGAGAAATATTAGAAACGGGACTGTTTGAGGAACTGAATGAC 1605
Db |||||
QY 1887 CCCAACAGACCTTACCGGTTGTGAGAGGGTAAATTCATCAAGTCTGGCGTGTGTTGTTA 1946
Db |||||
QY 1606 CCCAACAGACCTTACCGGTTGTGAGAGGGTAAATTCATCAAGTCTGGCGTGTGTTGTTA 1665
Db |||||
QY 1947 TTGTAATTTGCTCTCTTTTACCAGACAGCAGCAGGA 1982
Db |||||
QY 1666 TTGTAATTTGCTCTCTTTTACCAGACAGCAGCAGGA 1701
Db |||||

RESULT 13
US-09-802-117-3
; Sequence 3, Application US/09802117
; Publication No. US20020042503A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444561 Human G-Coupled Protein Receptor Kinases and Polynu
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-3

Query Match 47.6%; Score 1046.8; DB 9; Length 1062;
Best Local Similarity 99.8%; Pred. No. 2.6e-305;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGCTGACATGCGGGGCTTGGACAACTGATGCCAACACCGGCTTACCTGCGAGGCCGG 350
Db 1 ATGCTGACATGCGGGGCTTGGACAACTGATGCCAACACCGGCTTACCTGCGAGGCCGG 60

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Db 61 AAGCCCTCGACTCGACACAGCAAGAGCTGACGCGGCGGCGGTAGCCTGGCCCTGCC 120

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Db 121 GGGCTGAGGGCTGCGCGAGCTCCGCCAGAGCTGTCCCTGAACTTCCACAGCCTGTG 180

QY 471 GAGCAGAGCCCATCGTTCGCGGCTTCTCGGTGACTTCTAGGCAAGTCCACAGTCC 530
Db 181 GAGCAGAGCCCATCGTTCGCGGCTTCTCGGTGACTTCTAGGCAAGTCCACAGTCC 240

QY 531 CGCAAGCGCGCAACTTCTTCCTAGAGGAGCTGACAGAACTGGGAGCTGGCCGAGGAGGCC 590
Db 241 CGCAAGCGCGCAACTTCTTCCTAGAGGAGCTGACAGAACTGGGAGCTGGCCGAGGAGGCC 300

QY 591 ACCAAGAGAGCGGCTGACAGGGCTGGTGGCCACTTGTGCGAGTGCCTGCCCCGGGG 650
Db 301 ACCAAGAGAGCGGCTGACAGGGCTGGTGGCCACTTGTGCGAGTGCCTGCCCCGGGG 360

QY 651 AACCCGCAACCTTCTTCAGCAGGCGGTGGCCACCAAGTGGCCAGCAGCCACCTGAG 710
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QY 771 CAGCCCTTTAAGGATTTGCTGACCGGCTTCTACGACAGTTCCTGCAAGTAACTC 830
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Db 541 TTCGAGATCAACCAAGTGTGACAGAAAGTACTTCACTGAGTTCAGAGTGTGCGGAAAGGT 600
Qy 891 GGTTTTGGGAGGATGTGCTCCGTCAGGTGAAACACATCGGAAAGATGTATGCTGTAAAG 950
Db 601 GGTTTTGGGAGGATGTGCTCCGTCAGGTGAAACACATCGGAAAGATGTATGCTGTAAAG 660
Qy 951 AAATCGGACAGNAGCGGCTGAGAGAAAGTGGCGAAGATGGCTCTCTTGGNAAAG 1010
Db 661 AAATCGGACAGNAGCGGCTGAGAGAAAGTGGCGAAGATGGCTCTCTTGGNAAAG 720
Qy 1011 GAAATCTTGGAGAAGTCAAGAGCCCTTTCAATGTCTCTGCGCTATGCTCTTGGAGGC 1070
Db 721 GAAATCTTGGAGAAGTCAAGAGCCCTTTCAATGTCTCTGCGCTATGCTCTTGGAGGC 780
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Db 1021 ATGAAGGTGGCAAGCCCATACCCAGAGG 1050

RESULT 14
US-10-217-745-3
; Sequence 3, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgenowski, Nathaniel L.
; TITLE OF INVENTION: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases an
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-3
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Query Match 47.6%; Score 1046.8; DB 14; Length 1062;
Best Local Similarity 99.8%; Pred. No. 2.6e-305;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 291 ATGTGGACATCGGGGCTGGACAACTGATCGGCAACACCGCTTACCTGAGGCCGG 350
Db 1 ATGTGGACATCGGGGCTGGACAACTGATCGGCAACACCGCTTACCTGAGGCCGG 60
Qy 351 AAGCCCTCGGACTGCGACAGCAAGAGTGCAGCGCGCGCGGTAGCCTGCGCCCTGCC 410
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; Sequence 3, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
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Db 121 GGGCTGCAAGGGTGCAGCGAGCTCGCGCAGAAAGTGTCTCCCTGAACCTTCCACAGCCTGTGT 180
Qy 471 GAGCAGAGCCCATCGGTGCGCGCTTCTTCGTGACTTCTTAGCCACAGTGGCCACCTTC 530
Db 181 GAGCAGAGCCCATCGGTGCGCGCTTCTTCGTGACTTCTTAGCCACAGTGGCCACCTTC 240
Qy 531 CGCAAGGCGGCAACCTTCTTAGAGAGAGCTGCAGAACTGGGAGCTGGCCGAGGAGGCC 590
Db 241 CGCAAGGCGGCAACCTTCTTAGAGAGAGCTGCAGAACTGGGAGCTGGCCGAGGAGGCC 300
Qy 591 ACCAAGAGCAGCGCGCTGAGGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCGCCCGGG 650
Db 301 ACCAAGAGCAGCGCGCTGAGGGGCTGTGGCCACTTGTGCGAGTGGCCCTGCGCCCGGG 360
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Db 361 AACCCGCAACCTTCTCAGCAGCGCGCTGCGCCACTCAAGTGCACAGCAGCCACCTGAG 420
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Db 601 GGTTTTGGGAGGATGTGCGCTCAGGTGAAAAACACTGCGGAAAGATGTATGCTGTAAAG 660
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Db 661 AAATCGGACAGNAGCGGCTGAGAGAAAGTGGCGAAGATGGCTCTCTTGGNAAAG 720
Qy 1011 GAAATCTTGGAGAAGTGCAGACCGCTTCAATGTCTCTCTGCGCTATGCTTTCAGAGC 1070
Db 721 GAAATCTTGGAGAAGTGCAGACCGCTTCAATGTCTCTCTGCGCTATGCTTTCAGAGC 780
Qy 1071 AAGACCCATCTCTGCTTGTATGAGCCCTGATGAATGGGGAGACCTCAAGTTTCCACATC 1130
Db 781 AAGACCCATCTCTGCTTGTATGAGCCCTGATGAATGGGGAGACCTCAAGTTTCCACATC 840
Qy 1131 TACAAGTGGGACCGGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 1190
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Db 1021 ATGAAGGTGGCAAGCCCATACCCAGAGG 1050
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; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000638DIV
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

Query Match 39.5%; Score 867.4; DB 9; Length 36651;
Best Local Similarity 95.1%; Pred. No. 3.9e-250;
Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GRACCTAAGATGAAGGACCTCACTATAGGCTCGAGCGCGCGCGGCGAGTGTTC 60
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QY 181 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCGGGAAGGAAAGCAGCCAGCA 240
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